

FIGURE 1

OLIGODEOXYNUCLEOTIDE SEQUENCE FOR 5' SIDE PRIMER

Primer HS-1

CGTGGCCATCCTGGGCAACACCCTG

G C G G CT
 G
 T

HTRHR	CCTGGGCATTGTAGGCAACATCATGGT
HUMRANTES	CATTGGCCTGGTTGGAAACATCCTGGT
HSBLR1A	CCTGGGCGTGATCGGCAACGTCCTGGT
HUMSOMAT	GGTGGGGCTGGTGGGCAACGCCCTGGT
RNU02083	AGTGGGCCTCTTCGGAAACTTCCTGGT
U00442	GGTGGGCTTAGTGGGCAATTCCCTGGT
HUMNMBR	CGTGGGCTTGCTGGGCAACATCATGCT
HSHM4	GGTGACCATCATCGGCAACATCCTGGT
RATAADRE01	CTTTGCCATCGTGGGCAACATCTTGGT
HUMSSTR3X	GGTGGGCCTGCTGGGTAACCTCGCTGGT
HUMC5AAR	GGTGGGAGTGCTGGGCAATGCCCTGGT
HUMRDC1A	CATCGGCATGATTGCCAACTCCGTGGT
HUMOPIODRE	CGTGGCGGTGCTCGGCAACCTCGTGGT
RATA2BAR	GCTGGCAGTGGCGGGCAACGTGCTGGT

FIGURE 2

OLIGODEOXYNUCLEOTIDE SEQUENCE FOR 3' SIDE PRIMER

Complementary Sequence TTTGCCATCTGCTGGATGCCCCACAAC
to Primer HS-2

C C TTT C
 G G
 T T

HUMSGIR	TTTGCCCTCTGCTGGTTCCTCTCAAC
HUMBOMB3S	TTTGCCCTCTGCTGGTTGCCAAATCAC
S46950	TTTGCCCTCTGCTGGCTGCCCTACAC
MUSGPCR	TTTGCCCTCGTCTGGTGCCCTCTCAAC
S43387	TTTGCCCTTTTATGGATGCCCTACAGG
RATNEURA	TTTGCCATCTGCTGGCTGCCCTATCAC
RATA1ARA	TTTGCCCTCAGCTGGCTGCCGCTGCAT
HUMOPIODRE	TTTGCCATCTGCTGGCTGCCCTATCAC
HUMNEKAR	TTTGCCATCTGCTGGCTGCCCTACCAC
RATADENREC	TTTGCCTTGTGCTGGCTGCCTTTGTCC
HUMSRI1A	TTTGTCATCTGCTGGATGCCTTTCTAC
S8637154	TTTGCTATCTGCTGGCTGCCCTATCAT
RNCGPCR	TTTGCCGCCTGCTGGATGCCTTTTACC
HUMSSTR4Z	TTTGTGCTCTGCTGGATGCCTTTCTAC
RATGNRHA	TTTGCACTGGTCGAAGCCAGACAAA

FIGURE 3

OLIGODEOXYNUCLEOTIDE SEQUENCE FOR 5' SIDE PRIMER

Primer 3A

CTGACCGCTCTIACIACTGACCGATAC

T T GG GT A C
G

Primer 3B

CTGACCGCTCTIACIACTGACCGATAT

T T GG GT A C
G

L11064	CTCACCATGATGAGCGTGGACCGCTAC
L11065	TTGACCATGATGGAGTGTGACCGCTAC
D16349	CTCTGCACCATGAGCGTGGACCGCTAC
X69676	CTGATGCTCGTGAGTATCGACCGCTAC
M35328	CTTACGGCACTGTCAGCTGACAGGTAC
M73482	CTCACTGCCCTCAGCGCCGACAGGTAC
M73481	CTCACGGCGCTCTCGGCAGACAGATAC
L08893	TTAACAATTCTCAGCGCTGACAGATAC
X62933	ATGACCGCCATCGCCGCTGACAGGTAC
X62934	ATGACAACCTGTGGCCTTTGACAGATAC
J05189	ATGACAGCCATTGCAGTGGACAGGTAT
M60786	CTCTGCGCTCTCAGTGTGGACAGGTAC
L04672	CTCACCTGCCTCAGCATTGACCGCTAC
X61496	TTGCTGGCTATCACTGTGGACCGCTAC
X59249	TTGCTGGCCATTGCTGTAGACCGATAC
L09249	CTCACCTGCCTCAGCATTGACCGCTAC
P30731	CTGACAGCTATCGCAGTGGACCGCCAC
M31210	CTCCTCGCCATCGCCATTGAGCGCTAT
U03642	CTCACCGGCCTCAGCTTCGACCGCTAC

FIGURE 4

OLIGODEOXYNUCLEOTIDE SEQUENCE FOR 5' SIDE PRIMER

Primer 3C CTCGCCGCTATIAGCATGGACCGITAC
 G CC G T T

Primer 3D CTCGCCGCTATIAGCATGGACCGITAT
 G CC G T T

L32840	ATTACCTGCATGAGTGTCGATAGGTAC
X64052	CTCACGTGTCTCAGCATCGATCGCTAC
M90065	CTCACGTGTCTCAGCATCGATCGCTAC
M91464	CTCACGTGTCTCAGCATTGATCGATAC
M88096	CTGGTAGCCATCTCTCTGGAGAGATAT
M99418	CTCGTGGCCATAGCCCTGGAGCGATAC
L04473	CTCGTGGCCATCGCACTGGAGCGGTAC
M73969	CTGGCCTGCATCAGTGTGGACCGTTAC
X65858	TTGGCCTGCATCAGTGTGGACCGTTAC
S46665	CTGGCTACCATTAGTGCCGACCGTTTC
M60626	ATCGCCCTCATTGCTCTGGACCGCTGT

FIGURE 5

OLIGODEOXYNUCLEOTIDE SEQUENCE FOR 3' SIDE PRIMER

Complementary Sequence TTTACCITCTGTTGGICGCCCTACCACATC
to Primer 6A GT TC T T

Complementary Sequence TTCACCITCTGTTGGICGCCCTACCACATC
to Primer 6B GT TC T T

L11064	TTCGTGGTGTGCTGGGCGCCCATCCACATC
L11065	TTCATCATCTGTTGGACCCCCATTACATC
D16349	TTTATCGTCTGCTGGACCCCCATCCACATC
X69676	TTTGTGCTGTGTTGGGTGCCTTTCCAGATC
M35328	TTTGCCTTCTGCTGGCTCCCCAACCATGTC
M73482	TTCATCTTCTGTTGGTTTCCAAACCACATC
M73481	TTGCGCTTCTGCTGGCTCCCCAATCATGTC
L08893	TTTGCCCTCTGCTGGTTGCCAAATCACCTC
X62933	TTTGCCATCTGCTGGCTGCCCTACCACCTC
X62934	TTGCGCATCTGCTGGCTGCCCTTCCACATC
J05189	TTTGCCATCTGCTGGCTGCCCTATCACGTG
M60786	TTGCGCCTGTGCTGGTTCCCTCTTCACTTA
L04672	TTTGTCTATCTGCTGGCTGCCCTACCACGTG
X61496	TTTGCCGCCTGCTGGATGCCTTTTACCCTC
X59249	TTTGCCCTTGTGCTGGCTGCCTTTGTCCATC
L09249	TTTGCCATCTGCTGGCTGCCCTACCACGTG
P30731	TTTGCCCTCTGCTGGTTCCCTCTCAACTGC
M31210	TTCATCGCCTGCTGGGCACCGCTCTTCATC
U03642	TTTGCCCTGTGCTGGATGCCCTACCACCTG

FIGURE 6

OLIGODEOXYNUCLEOTIDE SEQUENCE FOR 3' SIDE PRIMER

Complementary Sequence TTTTTCITTTGCTGGITTCCTACCACATG
to Primer 6C : CC T G C T T

L32840	TTCATCATTTGCTGGCTTCCCTTCCATGTT
X64052	TTCTTCTTTTCCTGGGTTCCCCACCAAATA
M90065	TTCTTCTTTTCCTGGGTTCCCCACCAAATA
M91464	TTTTTCTTTTCCTGGATTCCCCACCAAATA
M88096	TTCTTCCTGTGCTGGATGCCCATCTTCAGC
M99418	TTCTTCCTGTGTTGGCTGCCAGTGTACAGC
L04473	TTTTTCTGTGTTGGTTGCCAGTTTATAGT
M73969	TTCTGCTTTGCTGGCTGCCCTACAACCTG
X65858	TTCTGCTTTGCTGGCTGCCCTACAACCTG
S46665	TTCTTTATCTTCTGGCTGCCCTATCAGGTG
M60626	TTTTTCTCTGCTGGTCCCCATATCAGGTG

FIGURE 7

OLIGODEOXYNUCLEOTIDE SEQUENCE FOR 5' SIDE PRIMER

Primer T2A

GTCACCAACITGTTTCATCCTCAICCTG

C

AC

GT T

A

HUMGALAREC

ACCACCAACCTGTTTCATCCTCAACCTG

RATADRA1B

CCCACCAACTACTTTATCGTCAACCTG

HUMADRB1

ACCACCAACCTGTTTCATCCTCAACCTG

RABIL8RSB

GTCACCGACGTCTACCTGCTGAACCTG

HUMOPIODRE

GTCACCAACTCCTTCCTCGTGAACCTG

BTSKR

GTGACCAACTACTTCATCGTCAACCTG

HUMSRI2A

ATCACCAACATTTACATCCTCAACCTG

HUMSSTR3Y

GTCACCAACGTCTACATCCTCAACCTG

HUMGARE

GTCACCAACGCCTTCCTCCTCTCACTG

HUMCCKAR

GTCACCAACATCTTCCTCCTCTCCCTG

HUMSHTR

CCCTCCAACCTACCTGATCGTGTCCCTG

HUMD1B

ATGACCAACGTCTTCATCGTGTCTCTG

HUM5HT1E

CCTGCCAACTACCTAATCTGTTCTCTG

HUMD4C

CCCACCAACTCCTTCATCGTGAGCCTG

MMSERO

GCCACCAACTATTTCTGATGTCACTT

RATADRA1A

GTCACCAACTATTTTCATCGTGAACCTG

S57565

CTGACCAATTGCTTCATTGTGTCCCTG

FIGURE 8

COMPLEMENTARY OLIGODEOXYNUCLEOTIDE SEQUENCE TO 3' SIDE PRIMER

Complementary Sequence A A C C C C I T C I T C T A T T G C T T T I T C I C T
to Primer T7A T T C C C G G

HUMGALAREC	AATCCTATCATTTATGCATTTCTCTCT
RATA1ADREC	AACCCCATCGTCTATGCCTTCCGGATC
PIGA2R	AATCCTCTCTTTTATGGCTTTCTGGGG
RAT5HTRTC	AACCCTATCATCTACCCGCTCTTTATG
S58541	AACCCCATCATTTATGCCTTTAATGCT
HUMGRPR	AACCCCTTTGCCCTCTACCTGCTGAGC
MUSGRPBOM	AACCCCTTTGCTCTTTATCTGCTGAGC
RRVT1AIIR	AACCCCTCTGTTCTACGGCTTTCTGGGG
HUMADRB1	AACCCCATCATCTACTGCCGCAGCCCC
HSHM4	AACCCCGTGTGCTATGCTCTGTGCAAC
HUMGARE	AACCCCTGGTCTACTGCTTCATGCAC
RATCCKAR	AACCCCATCATCTATTGCTTCATGAAC
S59749	AATCCCATGCTCTACACCTTCGCTGGC
HUMSST28A	AACCCCGTCCTCTACGGCTTCCTCTCG
RNGPROCR	AACCCCATCCTCTACGGCTTCCTCTCC
MUSSSRI1A	AACCCCATACTCTACGGCTTCCTGTCTG
HUMA1AADR	AACCCGCTCATCTACCCCTGTTCCAGC
S66181	AACCCGGTTCTCTACGCCTTCCTGGAC
HUMSSTR3Y	AACCCCATCCTTTATGGCTTCCTCTCC

FIGURE 9

OLIGODEOXYNUCLEOTIDE SEQUENCE FOR 5' SIDE PRIMER

Primer TM1-A2

TGITGGTTATIGGIGTTGTIGGIAA

CC GC C G

MUSBB2R	TGGTGGTGGTGGTGGTGGTGGGCAA
BTSKR	TGGTGCTGGTGGCTGTGATGGGCAA
BOVEETBR	TGTTTCGTGCTGGGCATCATCGGAAA
HUMNEUYREC	TGATCATTCTTGGTGTCTCTGGAAA
MMSUBKREC	TGGTGCTGGTGGCTGTAACAGGCAA
HUMPGE2R	TGTTTCATCTTCGGGGTGGTGGGCAA
HUMPIR	TGTTTCGTGGCCGGTGTGGTGGGCAA
HSU11053	TGTTTCGTGCTGGGCTTGGTGGGCAA
RRMC3RA	TGGTGATCCTGGCTGTGGTGAGGAA
HUMMR	TGGTTATCCTGGCCGTGGTCAGGAA
MUSGRPBOB	TCATCGTGATAGGTCTTATTGGCAA
RATCHOLREC	TCTTTCTGATGAGTGTTGGCGGAAA
RATCCKAR	TATTCCTTCTCAGTGTGCGGGGGAA

FIGURE 10

COMPLEMENTARY OLIGODEOXYNUCLEOTIDE SEQUENCE TO 3' SIDE PRIMER

Complementary Sequence GCCATACCITGGACAGATACCGAT
to Primer TM3-B2 A T A C G A G

HUMCCKR	GCCATCGCACTGGAGCGGTACAG
HUMCCKBGR	GCCATCGCACTGGAGCGGTACAG
MMGMC5R	GCCATTGCGGTGGACAGGTACA
HUMV2R	GCCATGACGCTGGACCGCCACCG
RATNEURA	GCCATTGCAGTGGACAGGTA
DOGGSTRN	GCCATCGCCCTGGAGCGATACAG
RAT5HT5A	GCAATAGCTTTGGACCGCTACTGGT
MUSALP2ADA	GCCATTAGTCTGGACCGCTACTGGT
HUMADORA1X	GCAATTGCTGTGGACCGCTACC
HUMOPIODRE	GCCATCGCGGTGGACAGATACA
MUSGRP BOM	GCACTGTCAGCTGACAGGTACAAA
RATCCKAR	GCCATCTCTCTGGAGAGATATGG
HSTRHREC	GCCTTTACCATTGAGAGGTACATA

FIGURE 11

OLIGODEOXYNUCLEOTIDE SEQUENCE FOR 5' SIDE PRIMER

Primer TM3-C2

CATGGCCGTGGAGAGITACITGGC

TT C C T A

HUMNK3R

CATTGCGGTGGACAGGTATATGGC

HSMRNOXY

CATGTCCCTGGACCGCTGCCTGGC

S68242

CATATCGCTGGAGAGATACGGAGC

CFGPCR4

CATCGCTCTGGACAGGTACTGGGC

MMSUBPREC

TGGCCTTTGACAGATACATGGC

HUMOPIODRE

CATCGCGGTGGACAGATACATGGC

HUMGALAREC

ATGTCCGTGGACCGCTACGTGGC

HSS31G

CATTGCCCTGGACAGGTACTGGGC

HUMARB3A

CCTGGCCGTGGACCGCTACCTGGC

HUMHPR

CATGGCCGTGGAGCGCTGCCTGGC

RATCCKAR

CATCTCTCTGGAGAGATATGGCGC

FIGURE 12

COMPLEMENTARY OLIGODEOXYNUCLEOTIDE SEQUENCE TO 3' SIDE PRIMER

Complementary Sequence TTTGCCITCTGCTGGATCCCCAAC
to Primer TM6-E2 C G C G TT

HUMNEKAR	TTTGCCATCTGCTGGCTGCCCTAC
HUMSUBPRA	TTCGCCATCTGCTGGCTGCCCTTC
RATSKR	TTTGCCATCTGCTGGCTGCCCTAC
MUSGRPBOM	TTTGCCCTTCTGCTGGCTCCCCAAC
HUMOPIODRE	TTTGCCATCTGCTGGCTGCCCTA
HUMA2XXX	TTTGCCCTCTGCTGGCTGCCCCCT
HUMADRBR	TTCACCCTCTGCTGGCTGCCCTTC
CFGPCR8	TTCGCCCCCTCTGTGGCTGCCCCCT
HUMETSR	TTTGCCCTCTGCTGGCTTCCCCT
MMNPY1CDS	TTCGCCGTCTGCTGGCTGCCCCCT
HSMRNOXY	TTCATCGTGTGCTGGACGCCTTTC
RATCCKAR	TTCTTCCTGTGCTGGATGCCCATC

FIGURE 13

OLIGODEOXYNUCLEOTIDE SEQUENCE FOR 5' SIDE PRIMER

Primer TM2F18

ARYYTIGCIITIGCNGAY

HUMTSHX	AACCTGGCCTTTGCGGAT
HUMNEKAR	AATCTGGCGCTGGCTGAC
HUMFMLP	AACCTGGCCGTGGCTGAC
HUMINTLEU8	AACCTAGCCTTGGCCGAC
HUMATAADR	AACCTGGCCGTGGCCGAC
HUMIL8RA	AACCTGGCCTTGGCCGAC
HSDD2	AGCCTCGCAGTGGCCGAC
HUMANTIR	AATTTAGCACTGGCTGAC
HUMSOMAT	AACCTGGCCGTAGCCGAC
HUMEL4REC	AGCTTGGCTGTGGCTGAT
HSTRHREC	AGCCTGGCAGTAGCTGAT
HSU07882	AACCTGGCCTTAGCCGAT

(R = A or G, Y = C or T, N = A, C, G or T, and
I = Inosine)

FIGURE 14

COMPLEMENTARY OLIGODEOXYNUCLEOTIDE SEQUENCE TO 3' SIDE PRIMER

Complementary Sequence TTYNYNNTNTGYTGGITICCI
to Primer TM6R21

HSBAR	TTCACCCCTCTGCTGGCTGCCC
HUMNEKAR	TTTGCCATCTGCTGGCTGCCC
HUMETN1R	TTTGCTCTTTGCTGGTTCCCT
HUMHISH2R	TTCATCATCTGCTGGTTTCCC
HUMA1AADR	TTCGTGCTCTGCTGGTTCCCT
HUMIL8RA	TTCTTGCTTTGCTGGCTGCCC
HUMNMBR	TTCATCTTCTGTTGGTTTCCT
HUMNKIRX	TTGCCATCTGCTGGCTGCCC
HUMSUBPRA	TTGCCATCTGCTGGCTGCCC
HUM5HT1DA	TTTATCATCTGCTGGCTGCCC
HUMPFPR2A	TTCTTCATCTGTTGGTTTCCC
HSDD2	TTCATCATCTGCTGGCTGCCC
HUMNEUYREC	TTTGCACTCTGCTGGCTCCCT
HUM2XXX	TTTGCCCTCTGCTGGCTGCCC
HUMBK2A	TTCATCATCTGCTGGCTGCCC
HUMFMLPX	TTCTTCATCTGTTGGTTTCCC
HUMSSTR3X	TTCTTGCTCTGCTGGATGCCC
HUMCCKR	TTTTTTCTGTGTTGGTTGCCA
HSNEURA	TTTGTGGTCTGCTGGCTGCCC

(Y = C or T, N = A, C, G or T, and I = Inosine)

FIGURE 15

OLIGODEOXYNUCLEOTIDE SEQUENCE FOR 5' SIDE PRIMER

Primer S3A	GCCTGITIAIGATGAGTGTGGAIAGIT
	C G C TC C

HUMGALAREC	CCCTGGCCGCGATGTCCGTGGACCGCT
S70057	GCCTCGTGGCCATCGCACTGGAGCGGT
S67127	ACCTCTGCGCTCTTAGTGTTGACAGGT
S44866	GTCTATGTGCTCTGAGTATTGACAGAT
HUMC5AAR	TCCTGGCCACCATCAGCGCCGACCGCT
HUMANTIR	TACTCACGTGTCTCAGCATTGATCGAT
HUMBK2A	TCCTGATGCTGGTGAGCATCGACCGCT
HSNEURA	ACGTGGCCAGCCTGAGTGTGGAGCGCT
HUMGRPR	CACTCACGGCGCTCTCGGCAGACAGAT
HUMFSRS	GCCTGACAGTCATGAGCGTGGACCGCT
HUMIL8RA	TGTTGGCCTGCATCAGTGTGGACCGTT
HUMNEKAR	CCATGACCGCCATTGCTGCCGACAGGT

OLIGODEOXYNUCLEOTIDE SEQUENCE FOR 5' SIDE PRIMER

FIGURE 16

COMPLEMENTARY OLIGODEOXYNUCLEOTIDE SEQUENCE TO 3' SIDE PRIMER

Complementary Sequence	TGGITICCCTACCACITITCAICATC
to Primer S6A	T T GG GT

HUMGALAREC	TGGCTGCCGCACACATCATCCATCTC
S70057	TGGTTGCCAGTTTATAGTGCCAACACG
S67127	TGGTTCCCTCTTCATTTAAGCCGTATA
S44866	TGGCTTCCCCTTCACCTCAGCAGGATT
HUMC5AAR	TGGTTGCCCTACCAGGTGACGGGGATA
HUMANTIR	TGGATTCCCCACCAAATATTCACTTTT
HUMBK2A	TGGCTGCCCTTCCAGATCAGCACCTTC
HSNEURA	TGGACTCCGTTCTCTATGACTTCTAC
HUMGRPR	TGGCTCCCAATCATGTCATCTACCTG
HUMFSRS	TGGCTGCCCTTCTTCACCGTCAACATC
HUMIL8RA	TGGCTGCCCTACAACCTGGTCCTGCTG
HUMNEKAR	TGGCTGCCCTACCACCTCTACTTCATC



FIGURE 18

A58-T7-2	10	20	30	40	50
	GTGGGCA	TGGTGGCA	ACCCCTGGT	CACTTCG	TGATCCTTCGCTACGC
HUMSOMAT	X:::	:::::	:::::	:::::	:::::
	GTGGGGCT	TGGTGGCA	ACGCCCTGGT	CACTTCG	TGATCCTTCGCTACGC
	285	295	305	315	325
A58-T7-2	60	70	80	90	100
	CAAGATGA	AAGACGGCTAC	CAACATCTAC	CTGCTCA	ACCTGGCCGTAAGCCG
HUMSOMAT	:::::	:::::	:::::	:::::	:::::
	CAAGATGA	AAGACGGCTAC	CAACATCTAC	CTGCTCA	ACCTGGCCGTAAGCCG
	335	345	355	365	375
A58-T7-2	110	120	130	140	150
	ACGAGCTC	TTCATGCTG	AGCGTGCCCTTC	GTGGCCCTCG	TGCGCCGCCCTG
HUMSOMAT	:::::	:::::	:::::	:::::	:::::
	ACGAGCTC	TTCATGCTG	AGCGTGCCCTTC	GTGGCCCTCG	TGCGCCGCCCTG
	385	395	405	415	425
A58-T7-2	160	170	180	190	200
	CGCCACTG	GCCCCTTCGG	CTCCGTGCTG	TGCCCGCGG	TGCTCAGCGTCGA
HUMSOMAT	:::::	:::::	:::::	:::::	:::::
	CGCCACTG	GCCCCTTCGG	CTCCGTGCTG	TGCCCGCGG	TGCTCAGCGTCGA
	435	445	455	465	475
A58-T7-2	210	220	230	240	
	CGGCCCTC	AACATGTTCA	CCAGCGTCTT	CTGTCTCA	CCGTGCTCAGCGT
HUMSOMAT	:::::	:::::	:::::	:::::	:::::
	CGGCCCTC	AACATGTTCA	CCAGCGTCTT	CTGTCTCA	CCGTGCTCAGCGT
	485	495	505	515	

FIGURE 19

A58-SP6	10	20	30	40	50
	CAGTGTCCACACCCGGCCTGGTCGGCAGTCTTCGTGGTCTACACTTTCCT				
HUMSOMATA	X:::	:::	:::	:::	:::
	CAGTGGCCACACCCGGCCTGGTCGGCAGTCTTCGTGGTCTACACTTTCCT				
	706	716	726	736	746
A58-SP6	60	70	80	90	100
	GCTGGGCTTCCGTGTCCCGTGTGTCATTTGGCCCTGTGTACCTGCTCA				
HUMSOMATA	:::	:::	:::	:::	:::
	GCTGGGCTTCCGTGTCCCGTGTGTCATTTGGCCCTGTGTACCTGCTCA				
	756	766	776	786	796
A58-SP6	110	120	130	140	150
	TCGTGGCAAGATGCGCGCGTGTCCCTGCGCGCTGGCTGGCAGCAGCGC				
HUMSOMATA	:::	:::	:::	:::	:::
	TCGTGGCAAGATGCGCGCGTGTCCCTGCGCGCTGGCTGGCAGCAGCGC				
	806	816	826	836	846
A58-SP6	160	170	180	190	200
	AGGCGCTCGGAGAAATCACCAGGCTGGTGTGATGGTGGTGGTGGT				
HUMSOMATA	:::	:::	:::	:::	:::
	AGGCGCTCGGAGAAATCACCAGGCTGGTGTGATGGTGGTGGTGGT				
	856	866	876	886	896
A58-SP6	210	220			
	CTTTGCCCTCTGCTGGTGGCTTCCAC				
HUMSOMATA	:::	:::	:::	:::	:::
	CTTTGTGCTCTGCTGGATGCCCTTCTAC				
	906	916			

		10	20	30	40	50
57-A-2		GTGGGCATGCTGGGCAACCTCCTGGAAGGCAGTCGCCGAGGTGGCCGGTT				
		X:::	:	:	:	:
HUMDRD5A		GTGGCGCTGCTGGTCATGC-CCTGGAAGGCAGTCGCCGAGGTGGCCGGTT				
		424	434	444	454	
		60	70	80	90	100
57-A-2		ACTGGCCCTTTGGAGCGTTCTGCGACGTCTGGGTGGCCTTCGACATCATG				
		:	:	:	:	:
HUMDRD5A		ACTGGCCCTTTGGAGCGTTCTGCGACGTCTGGGTGGCCTTCGACATCATG				
	464	474	484	494	504	
		110	120	130	140	150
57-A-2		TGCTCCACTGCCTCCATCCTGAACCTGTGCGTCATCAGCGTGGACCGCTA				
		:	:	:	:	:
HUMDRD5A		TGCTCCACTGCCTCCATCCTGAACCTGTGCGTCATCAGCGTGGACCGCTA				
	514	524	534	544	554	
		160	170	180	190	200
57-A-2		CTGGGCCATCTCCAGGCCCTTCCGCTACAAGCGCAAGATGACTCAGCGCA				
		:	:	:	:	:
HUMDRD5A		CTGGGCCATCTCCAGGCCCTTCCGCTACAAGCGCAAGATGACTCAGCGCA				
	564	574	584	594	604	
		210	220	230	240	250
57-A-2		TGGCCTTGGTCATGGTCGGCCTGGCATGGACCTTGTCATCCTCATCTCC				
		:	:	:	:	:
HUMDRD5A		TGGCCTTGGTCATGGTCGGCCTGGCATGGACCTTGTCATCCTCATCTCC				
	614	624	634	644	654	
		260	270	280	290	300
57-A-2		TTCATTCCGGTCCAGGTCAACTGGGACAGGGACCAGGCGGGCTCTTGGGG				
		:	:	:	:	:
HUMDRD5A		TTCATTCCGGTCCAGGTCAACTGGGACAGGGACCAGGCGGGCTCTTGGGG				
	664	674	684	694	704	
		310				
57-A-2		GGGGCTGGACCTGCCAAA				
		:	:	:	:	:
HUMDRD5A		CGGGCTGGACCTGCCAAA				
	714	724				

B54		10	20	30	40	50
		<u>G T G G C C A T C G T G G C C A C A C A T C C T G G T C A T A T T C G T G A T C C T A C G C T A T G C</u>				
RNU04738		X :				
		G T G G C C T G G T A G G A A A C G C C C T G G T C A T A T T C G T G A T C C T A C G C T A T G C				
		233	243	253	263	273
B54		60	70	80	90	100
		C A A A T G A A G A C A G C C A C C A C A C A T C T A C C T G C T C A A C C T G G C C G T C G C T G				
		: :				
RNU04738		C A A A T G A A G A C A G C C A C C A A C A T C T A C C T G C T C A A C C T G G C C G T C G C T G				
		283	293	303	313	323
B54		110	120	130	140	150
		A T G A G C T C T T C A T G C T C A G T G T G C C A T T T G T G G C C T C G G C G G C T G C C C T G				
		: :				
RNU04738		A T G A G C T C T T C A T G C T C A G T G T G C C A T T T G T G G C C T C G G C G G C T G C C C C T G				
		333	343	353	363	373
B54		160	170	180		
		C G C C A C T G G C C G T T C G G G C G G T G C T G T G C C G C				
		: X				
RNU04738		C G C C A C T G G C C G T T C G G G C G G T G C T G T G C C G C				
		383	393	403		

5'	9	18	27	36	45	54
GTG GGC ATG GTG GGC AAC GTC CTC CTG GTG CTG ATC GCG GTG CCG CGG	63	72	81	90	99	108
Val Gly Met Val Gly Asn Val Leu Leu Val Leu Val Ile Ala Arg Val Arg Arg						
CTG CAC AAC GTG ACG AAC TTC CTC ATC GGC AAC CTG GCC TTG TCC GAC GTG CTC						
Leu His Asn Val Thr Asn Phe Leu Ile Gly Asn Leu Ala Leu Ser Asp Val Leu						
ATG TGC ACC GCC TGC GTG CCG CTC ACG CTG GCC TAT GCC TTC GAG CCA CCG GGC	117	126	135	144	153	162
Met Cys Thr Ala Cys Val Pro Leu Thr Leu Ala Tyr Ala Phe Glu Pro Arg Gly						
TGG GTG TTC GGC GGC GTC TGC CAC CAC CTG GTC TTC TTC CTG CAG CCG GTC ACC	171	180	189	198	207	216
Trp Val Phe Gly Gly Gly Leu Cys His Leu Val Phe Phe Leu Gln Pro Val Thr						
GTC TAT GTG TCG GTG TTC ACG CTC ACC ACC ATC GAA GTG GAC CCG TAC GTC GGT	225	234	243	252	261	270
Val Tyr Val Ser Val Phe Thr Leu Thr Thr Ile Glu Val Asp Arg Tyr Val Gly						
GCT GGT GCA CCC GCT GAG GCG GCG CAT 3'	279	288	297			
Ala Gly Ala Pro Ala Glu Ala Gly His						

FIGURE 23

5'	9	18	27	36	45	54
GGC CTG CTG CTG	ACC TAC CTG	CCT CTG	CTG CTG	ATC ATC	CTC CTG	TCT TAC
---	---	---	---	---	---	---
Gly Leu Leu Val	Thr Tyr Leu Leu	Pro Leu Leu	Val Val	Ile Ile	Leu Leu	Ser Tyr
63	72	81	90	99	108	
GTC CGG GTG TCA	GTG AAG CTC	CGC AAC CCG	GTG GTG	TGC GTG	ACC CAG	
---	---	---	---	---	---	---
Val Arg Val Ser	Lys Leu Arg	Asn Pro Val	Val Val	Cys Val	Thr Gln	
117	126	135	144	153	162	
AGC CAG GCC GAC	TGG GAC CGC	GCT CGC CGC	CGC ACC	TTC TGC	TTG CTG	GTG
---	---	---	---	---	---	---
Ser Gln Ala Asp	Trp Asp Arg	Ala Arg Arg	Arg Arg	Thr Phe	Cys Leu	Val
171	180	189	198			
GTG GTC CTG CTG	TTT GCC ATC	TGC TGG	TTG CCT	TAC TAC	3'	
---	---	---	---	---	---	---
Val Val Val Val	Phe Ala Ile	Cys Trp Leu	Pro Pro	Tyr Tyr		

FIGURE 24

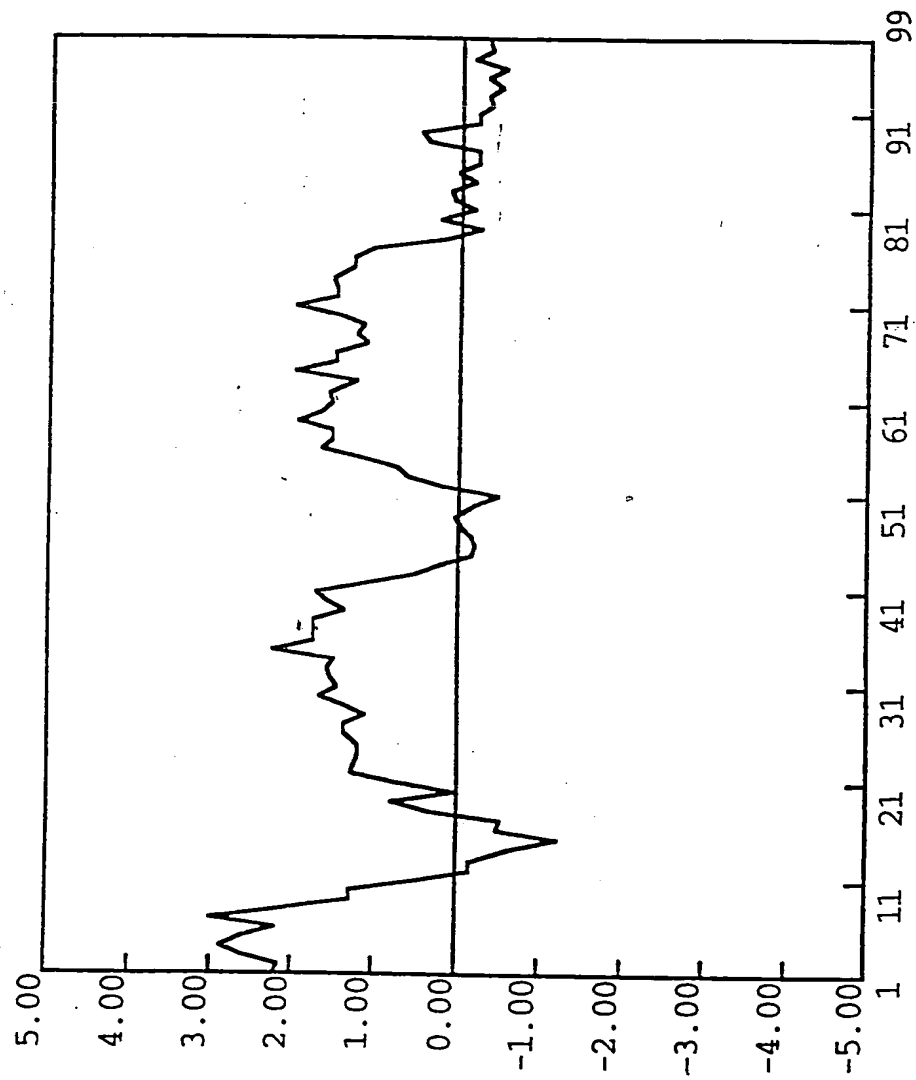


FIGURE 25

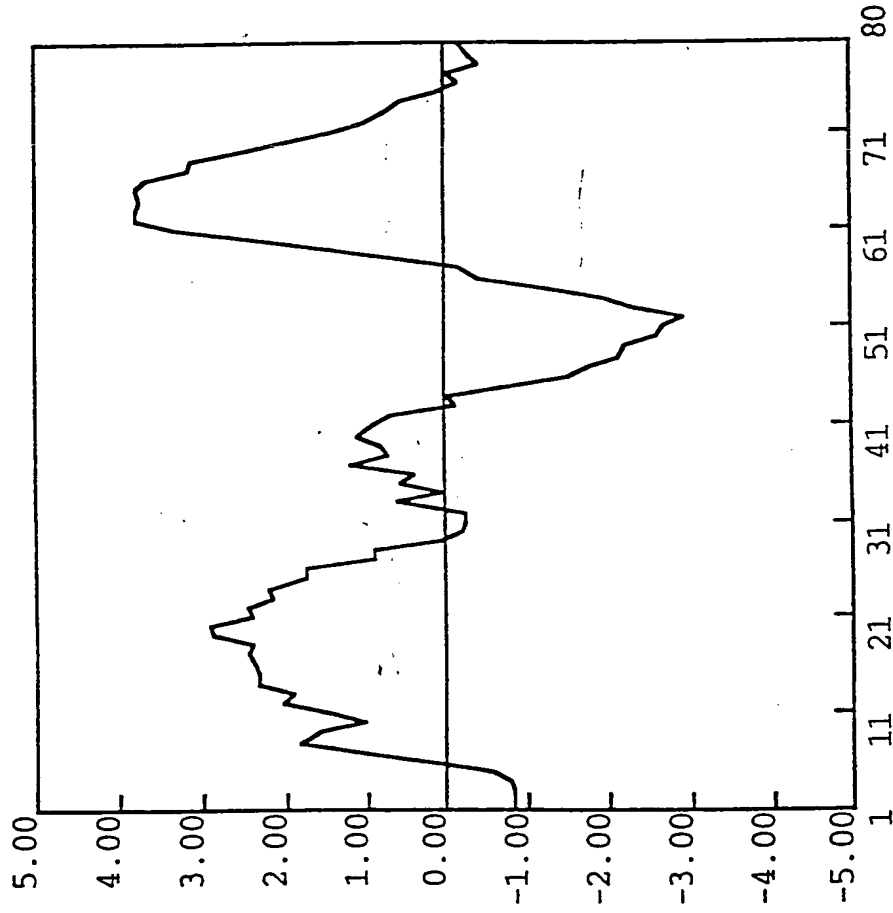


FIGURE 26

p19P2	1	10	20	30	40	50
		VGMVGNVLLV	LVIAVRRLH	NVTNFLIGNL	ALSDVLMCTA	CVPLTLAYAF
S12863	1	10	20	30	40	50
		LGVSIGNLALI	IIILKQKEMR	NVTNIIIVNL	SFSDILLVAVM	CLPFTFVYTL
p19P2	51	60	70	80	90	100
		EPRGWVFGGG	LCHLVFFLQP	VTVYVSVFTL	TTIEVDRYVG	AGAPAEAGH
S12863	51	60	70	80	90	100
		MDH-WVFGET	MCKLNPEVGC	VSITVSIFSL	VLIIVERHQL	IINPRGWRPN
p19P2	101	110	120	130	140	150
		NRHAYIGITV	IWVLAVASSL	PFVIYQILTD	EPFQNVSLAA	FKDKYVCFDK
S12863	101	110	120	130	140	150
		GLLV	TYLLPLLVIL	LS-----Y	VRSVKLRNPV	VPVCVTQSQ
p19P2	151	160	170	180	190	200
		GLLV	TYLLPLLVIL	LS-----Y	VRSVKLRNPV	VPVCVTQSQ
S12863	151	160	170	180	190	200
		FPDSHRLSY	TTLLLVQYF	GPLCFIFICY	FKIYIRLKRR	NNMMDKIRDS
p19P2	201	210	220	230	240	250
		DWDRARRRT	FCLVVVVVV	FAICWLPHY
S12863	201	210	220	230	240	250
		KYRSSETKRI	NVMLLSIVVA	FAVCWLPLT

FIGURE 27

		657			666		
CTC	TGC	TGG	CTG	CCC	TTC	TTC	3
---	---	---	---	---	---	---	
Leu	Cys	Trp	Leu	Pro	Phe	Phe	

FIGURE 28

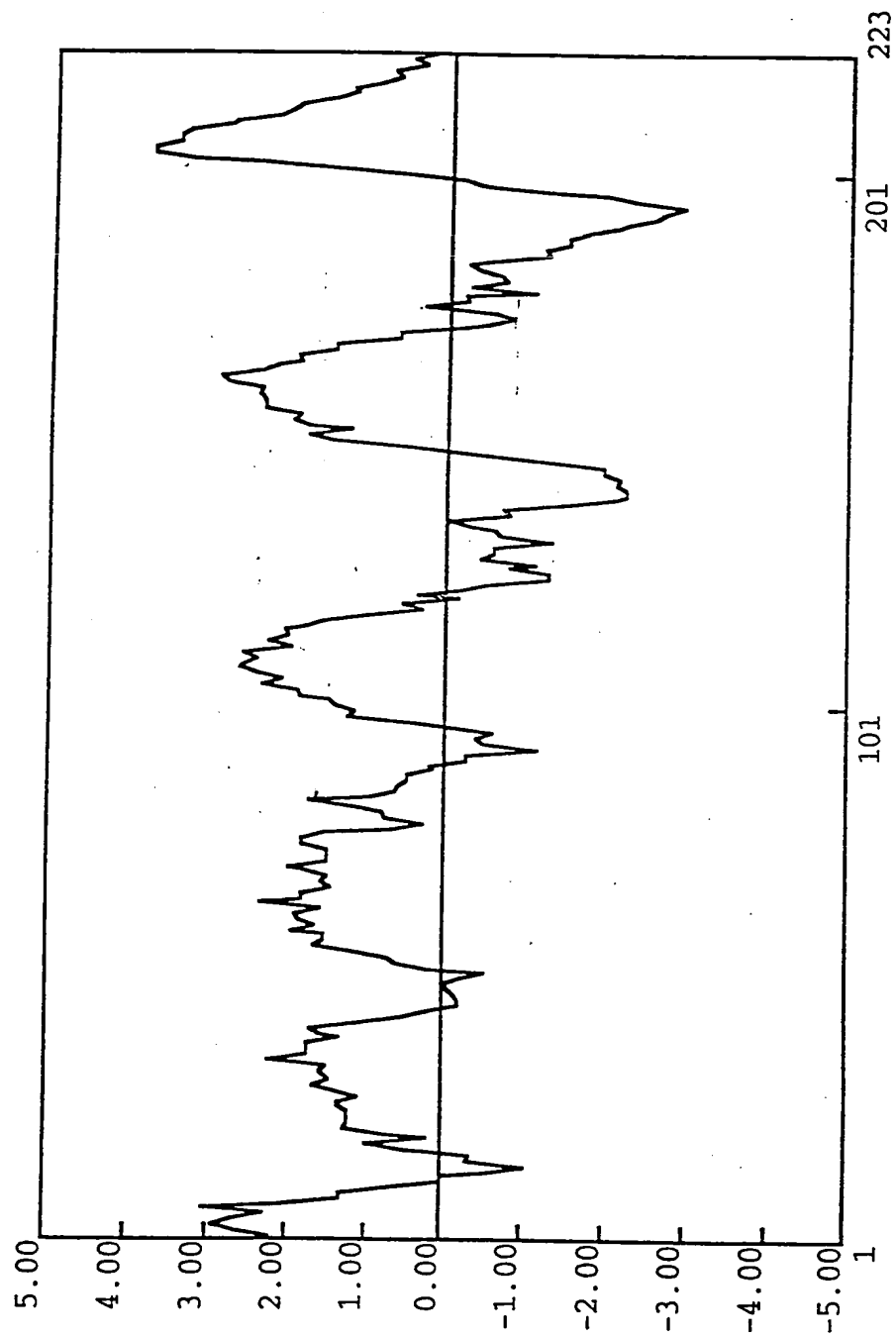


FIGURE 29

CAC	GTC	TCA	GCA	CTG	ACA	235
His	Val	Ser	Ala	Leu	Thr	226

FIGURE 30

5'	9	18	27	36	45	54
	GAG CCA GCT GAC CTC TTC TGG AAG AAC CTG GAC TTG CCC ACC TTC ATC CTC					
	---	---	---	---	---	---
	Glu Pro Ala Asp Leu Phe Trp Lys Asn Leu Asp Leu Pro Thr Phe Ile Leu Leu					
	63	72	81	90	99	108
	AAC ATC CTG CCC CTC CTC ATC ATC TCT GTG GCC TAC GTT CGT GTG ACC AAG AAA					
	---	---	---	---	---	---
	Asn Ile Leu Pro Leu Leu Ile Ile Ser Val Ala Tyr Val Arg Val Thr Lys Lys					
	117	126	135	144	153	162
	CTG TGG CTG TGT AAT ATG ATT GTC GAT GTG ACC ACA GAG CAG TAC TTT GCC CTG					
	---	---	---	---	---	---
	Leu Trp Leu Cys Asn Met Ile Val Asp Val Thr Thr Glu Gln Tyr Phe Ala Leu					
	171	180	189	198	207	216
	CGG CCC AAA AAG AAG ACC ATC ATC AAG ATG ATG TTG ATG CTG GTG GTA CTC CTC TTT					
	---	---	---	---	---	---
	Arg Pro Lys Lys Lys Lys Thr Thr Ile Lys Met Leu Met Leu Val Val Leu Phe					
	225	234				
	GCC CTC TGC TGG TTG CCT CTC GAC 3'					
	---	---	---	---	---	---
	Ala Leu Cys Trp Leu Pro Leu Asp					

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FIGURE 31

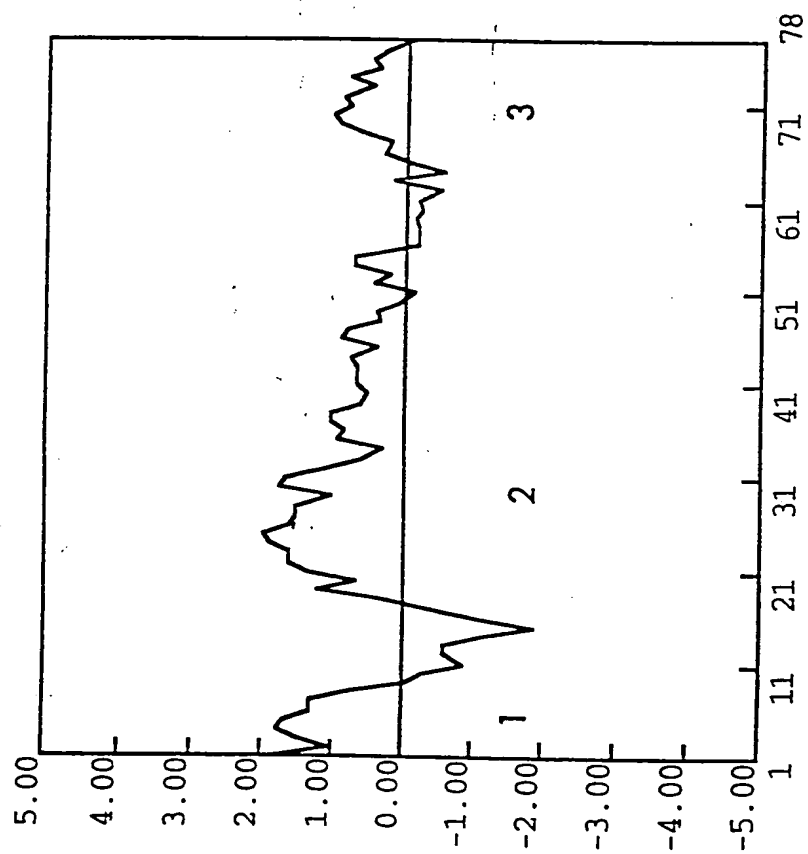


FIGURE 32

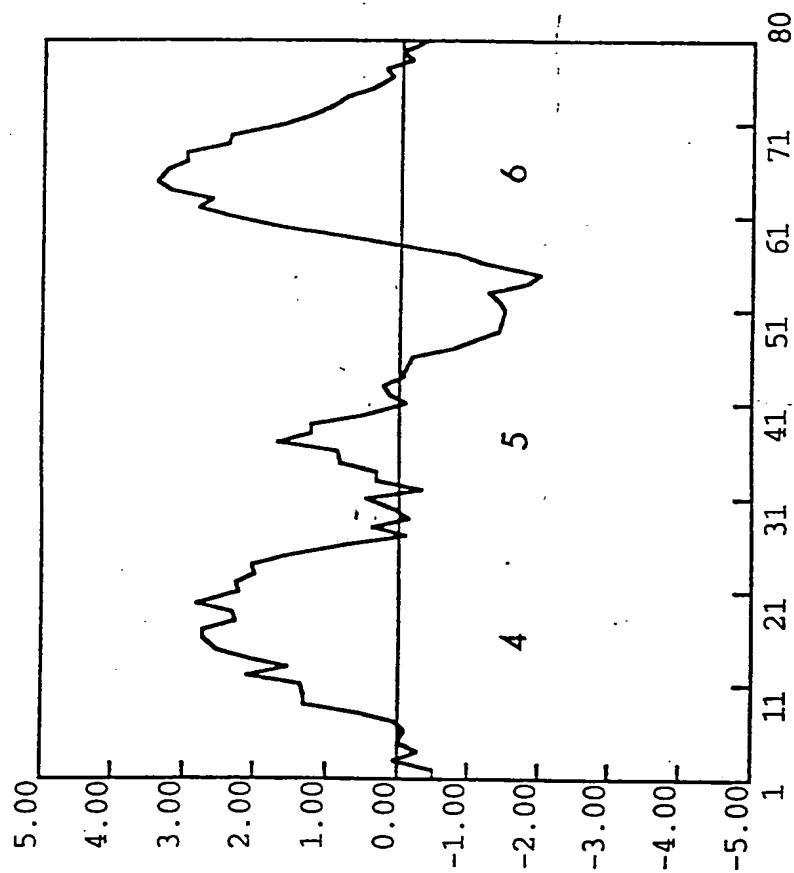


FIGURE 33

p63A2	1	10	20	30	40	50	
P30731	1	VCHVIFKNQR	MHSATSLFIV	NLAADIMIT	LNTPFTLVR	FVNSTWIFGK	50
	1	VCHVIFKNQR	MHSATSLFIV	NLAADIMIT	LNTPFTLVR	FVNSTWIFGK	50
p63A2	51	60	70	80	90	100	
P30731	51	GMCHVSRFAQ	YCSLHVSAIT	LTAIAVDRHQ	VIMHPLKPRI	SITKGVIIYA	100
	51	GMCHVSRFAQ	YCSLHVSAIT	LTAIAVDRHQ	VIMHPLKPRI	SITKGVIIYA	100
p63A2	101	110	120	130	140	150	
P30731	101	VIWVMATFFS	LPHAIQKLF	TFKYSEDIVR	SLCLPDFPER	ADLFWRNIDL	150
	101	VIWVMATFFS	LPHAIQKLF	TFKYSEDIVR	SLCLPDFPER	ADLFWRNIDL	150
p63A2	151	160	170	180	190	200	
P30731	151	PTFILLINILP	LLTISVAVWR	VTKKLWLCNM	IVDVITEQVF	ALRPKKKTI	200
	151	PTFILLINILP	LLTISVAVWR	VTKKLWLCNM	IVDVITEQVF	ALRPKKKTI	200
p63A2	201	210	220	230	240	250	
P30731	201	KMIMLVVVI.	250
	201	KMIMLVVVI.	250

FIGURE 34

1	CATCGTCAAGCAGATGAAGATCATCCACGAGGATGGCTACTCCGAGGGCCAGCAGAAATT	60
1		1
61	CTGCCCCCTTCTTCCCGGAGTGCTTTCCCGCTCTCCAAACCCCACTCCAGGTGGCCATG	120
1	Met	1
121	GCCTCATCGACCACTCGGGGCCCCAGGGTTTCTGACTTATTTCTGGGCTGCCGCCGGCG	180
1	AlaSerSerThrThrArgGlyProArgValSerAspLeuPheSerGlyLeuProProAla	21
181	GTCACAACCTCCCGCCAACCAGAGCGCAGAGGCTCGGCGGGCAACGGGTGGGTGGCTGGC	240
21	ValThrThrProAlaAsnGlnSerAlaGluAlaSerAlaGlyAsnGlySerValAlaGly	41
241	GCGGACGCTCCAGCCGTCACGCCCTTCAGAGCCTGCAGCTGGTGCATCAGCTGAAGGGG	300
41	AlaAspAlaProAlaValThrProPheGlnSerLeuGlnLeuValHisGlnLeuLysGly	61
301	CTGATCGTGTCTCTACAGCGTCTGGTGGTGGTGGGGCTGGTGGGCAACTGCCTGCTG	360
61	LeuIleValLeuLeuTyrSerValValValValValGlyLeuValGlyAsnCysLeuLeu	81
361	GTGCTGGTGATCGCGCGGGTGGCGGGCTGCACAACTGACGAACCTCTCTATCGGCAAC	420
81	ValLeuValIleAlaArgValArgArgLeuHisAsnValThrAsnPheLeuIleGlyAsn	101
421	CTGGCCTGTTCGACGTGCTCATGTGCACCGCCTGCGTGGCGCTCAGCTGGCCTATGCC	480
101	LeuAlaLeuSerAspValLeuMetCysThrAlaCysValProLeuThrLeuAlaTyrAla	121
481	TTGAGCCACGCGGCTGGGTGTTCGGCGCGCGGCTGTGCCACCTGGTCTTCTTCTGTCAG	540
121	PheGluProArgGlyTrpValPheGlyGlyGlyLeuCysHisLeuValPhePheLeuGln	141
541	CCGGTACCGTCTATGTGTGGTGTTCACGCTCACCACCATCGCAGTGGACCGCTACGTC	600
141	ProValThrValTyrValSerValPheThrLeuThrIleAlaValAspArgTyrVal	161
601	GTGCTGGTGCACCCGCTGAGGCGGCGCATCTCGCTGCGCCTCAGCGCCTACGCTGTGCTG	660
161	ValLeuValHisProLeuArgArgArgIleSerLeuArgLeuSerAlaTyrAlaValLeu	181
661	GCCATCTGGGCGCTGTCCGCGGTGCTGGCGCTGCCGCGCGCGTGACACCTATCACGTG	720
181	AlaIleTrpAlaLeuSerAlaValLeuAlaLeuProAlaAlaValHisThrTyrHisVal	201
721	GAGCTCAAGCCGACGACGTGCGCCTCTGCGAGGAGTTCTGGGGCTCCAGGAGCGCCAG	780
201	GluLeuLysProHisAspValArgLeuCysGluGluPheTrpGlySerGlnGluArgGln	221
781	CGCCAGCTCTACGCCTGGGGCTGTGCTGGTACCTACCTGCTCCCTCTGCTGGTCAATC	840
221	ArgGlnLeuTyrAlaTrpGlyLeuLeuLeuValThrTyrLeuLeuProLeuLeuValIle	241
841	CTCTGTCTTACGTCCGGGTGTCAGTGAAGCTCCGCAACCGCGTGGTGGCGGGCTGCGTG	900
241	LeuLeuSerTyrValArgValSerValLysLeuArgAsnArgValValProGlyCysVal	261
901	ACCCAGAGCCAGGCCGACTGGGACCGCGCTCGGCGCGCGCGCACCTTCTGCTGTGCTGGT	960
261	ThrGlnSerGlnAlaAspTrpAspArgAlaArgArgArgThrPheCysLeuLeuVal	281
961	GTGGTGGTGGTGGTGTTCGCGCTGCTGGCTGCCGCTGCACGTCTTCAACCTGCTGCGG	1020
281	ValValValValValPheAlaValCysTrpLeuProLeuHisValPheAsnLeuLeuArg	301
1021	GACCTCGACCCCCACGCCATCGACCTTACGCTTTGGGCTGGTGCAGCTGCTCTGCCAC	1080
301	AspLeuAspProHisAlaIleAspProTyrAlaPheGlyLeuValGlnLeuLeuCysHis	321
1081	TGGCTCGCCATGAGTTGGGCTGCTACAACCCCTTCATCTACGCTGGCTGCACGACAGC	1140
321	TrpLeuAlaMetSerSerAlaCysTyrAsnProPheIleTyrAlaTrpLeuHisAspSer	341
1141	TTCCGCGAGGAGCTGCGCAAACTGTGGTGGCTTGGCCCCGCAAGATAGCCCCCATGGC	1200
341	PheArgGluGluLeuArgLysLeuLeuValAlaTrpProArgLysIleAlaProHisGly	361
1201	CAGAATATGACCGTCAGCGTGGTCATCTGATGCCACTTAGCCAGGCCTTGGTCAAGGAGC	1260
361	GlnAsnMetThrValSerValValIle***	371
1261	TCCACTTCAACTGGCCTCCTAGGGCACCCTCGAGGTCAATCTGGTGTATTCTCAGCA	1320
371		371
1321	CCAGAGCTAGC	1331
371		371

FIGURE 35

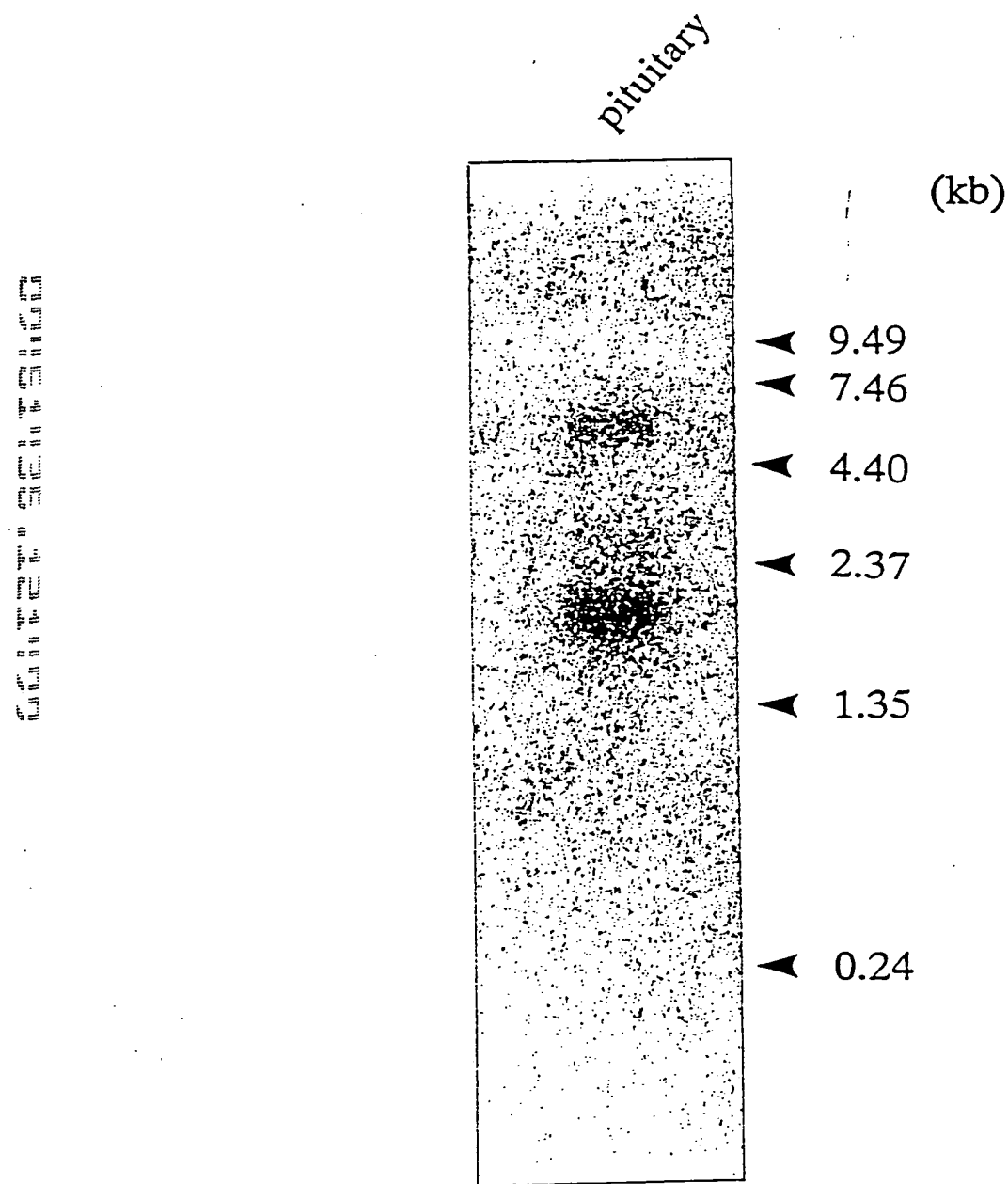
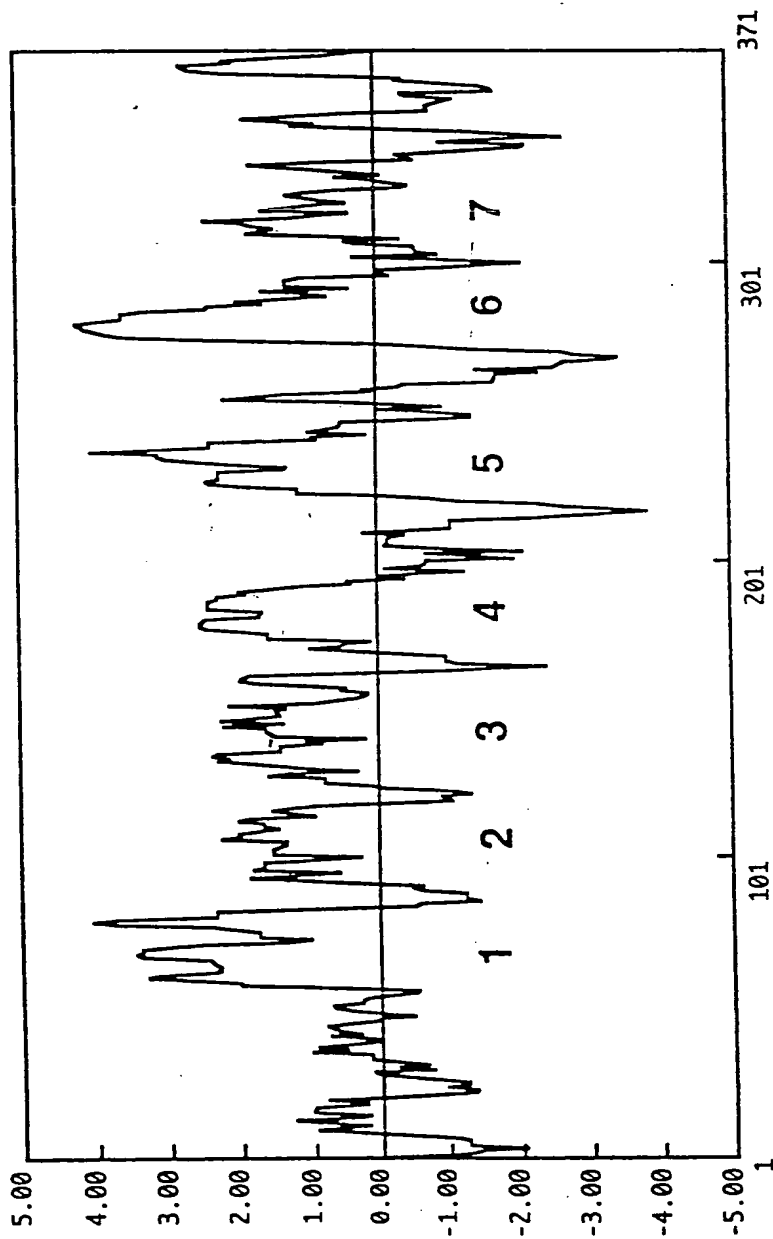
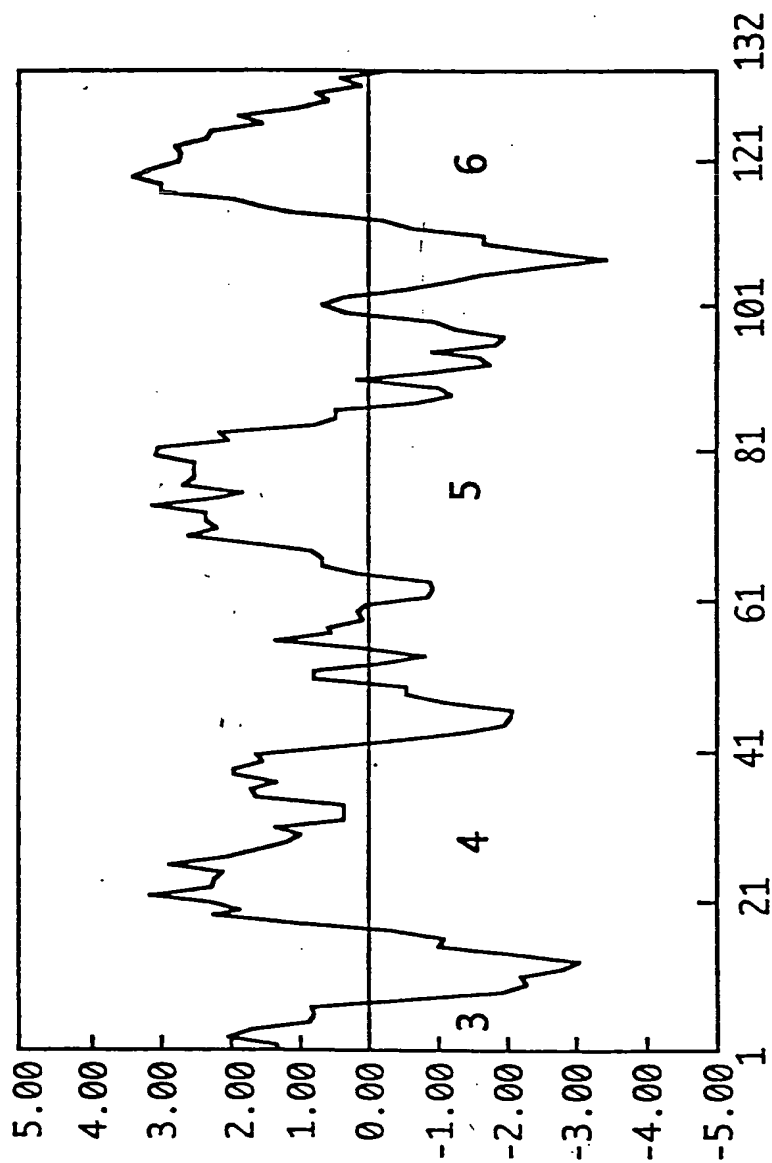


FIGURE 36



[illegible]

FIGURE 38



	10	20	30	40	50		
p3H2-17	1	VGLVGNILAS	WHKRGGRRAA	WVVCGVVWLA	VTAQC LPTAV	FAATG IQRN-	50
p34996	1	RYTG VVHPLK	SLGR LKKKNA	VYVSS LVMAL	VVAV IAPILF	YSGTG VRRN-	50
A46226	1	RYLAVVHPTR	SARWR TAPVA	RTVSA AAVWA	SAVVVL PVVV	F--SGVPRG-	50
JN0605	1	RYVAVVHPLR	AATYRRPSVA	KL I NLGVWLA	SLLVTL PIAL	FADTRPARGG	50
S28787	1	RYLAI VHATN	SKPKRKLAE	KVYVGVWLP	AVLLTI PDLI	FADIK EVD-	50
	60	70	80	90	100		
p3H2-17	51	RTIV-CYDL--	SPP I LSTRYL	PYGMALTVIG	FLLPFIALLA	CYGRMARRLC	100
p34996	51	KITTCYDT--	TAD EYLRSYF	VYSMCTTVFM	ECIPFIVILG	CYGLLVKALI	100
A46226	51	MST-CHMQWP	EPAAAWRAGE	I IY--TAA LG	FFGPLLVIICL	CYLLLVKVR	100
JN0605	51	QAVACNLQWP	HPAWSAVFVV	YTF----L LG	FLLPVLAIGL	CYLLLVGKVR	100
S28787	51	RYII-CDRF--	YPSDLWL VVE	QFQ--HIVVG	LLP GIVILS	CYGI IISKL S	100
	110	120	130	140	150		
p3H2-17	101	RQDGPA-GPV	AOE-RRS--K	AARM AVVVA	VFALCWLPLY	150
p34996	101	YKDLDN-SPL	---RR---K	S IYLV IIVLT	VFAVSYLPEH	150
A46226	101	SAGR RVWAPS	CORRRRSERR	VTRMVA AVVA	LFVLCWMPFY	150
JN0605	101	AVALLRA---G	WQORRRSEKK	ITRLVLMVVV	VFVLCWMPFY	150
S28787	101	HSKG-----	YOKR-----K	ALKTIVILIL	TFACWLPYY	150

FIGURE 40

5'	GTG	GGC	CTG	GTG	GGC	AAC	TTC	CTG	GCC	GCG	ATG	TCT	GTG	GAT	CGC	TAC	GTG	GCC	55
	Val	Gly	Leu	Val	Gly	Asn	Phe	Leu	Ala	Ala	Met	Ser	Val	Asp	Arg	Tyr	Val	Ala	
	ATT	GTG	CAC	TCG	CGG	CGC	TCC	TCC	TCC	CTC	AGG	GTG	TCC	CGC	AAC	GCA	CTG	CTG	109
	Ile	Val	His	Ser	Arg	Arg	Ser	Ser	Ser	Leu	Arg	Val	Ser	Arg	Asn	Ala	Leu	Leu	
	GGC	GTG	GGC	TTC	ATC	TGG	GCG	CTG	TCC	ATC	GCC	ATG	GCC	TCG	CCG	GTG	GCC	TAC	163
	Gly	Val	Gly	Phe	Ile	Trp	Ala	Leu	Ser	Ile	Ala	Met	Ala	Ser	Pro	Val	Ala	Tyr	
	CAC	CAG	CGT	CTT	TTC	CAT	CGG	GAC	AGC	AAC	CAG	ACC	TTC	TGC	TGG	GAG	CAG	TGG	217
	His	Gln	Arg	Leu	Phe	His	Arg	Asp	Ser	Asn	Gln	Thr	Phe	Cys	Trp	Glu	Gln	Trp	
	CCC	AAC	AAG	CTC	CAC	AAG	AAG	GCT	TAC	GTG	GTG	TGC	ACT	TTC	GTC	TTT	GGG	TAC	271
	Pro	Asn	Lys	Leu	His	Lys	Lys	Ala	Tyr	Val	Val	Cys	Thr	Phe	Val	Phe	Gly	Tyr	
	CTT	CTG	CCC	TCA	CTG	CTC	ATC	TGC	TTT	TGC	TAT	GCC	AAG	GTC	CTT	AAT	CAT	CTG	325
	Leu	Leu	Pro	Leu	Leu	Leu	Ile	Cys	Phe	Cys	Tyr	Ala	Lys	Val	Leu	Asn	His	Leu	
	CAT	AAA	AAG	CTG	AAA	AAC	ATG	TCA	AAA	AAG	TCT	GAA	GCA	TCC	AAG	AAA	AAG	ACT	379
	His	Lys	Lys	Leu	Lys	Asn	Met	Ser	Lys	Lys	Ser	Glu	Ala	Ser	Lys	Lys	Lys	Thr	
	GCA	CAG	ACC	GTC	CTG	GTG	GTC	GTT	GTA	GTA	TTT	GCC	CTC	TGC	TGG	CTG	CCT	TTT	433
	Ala	Gln	Thr	Val	Leu	Val	Val	Val	Val	Val	Phe	Ala	Leu	Cys	Trp	Leu	Pro	Phe	

TAC 3'

Tyr

FIGURE 41

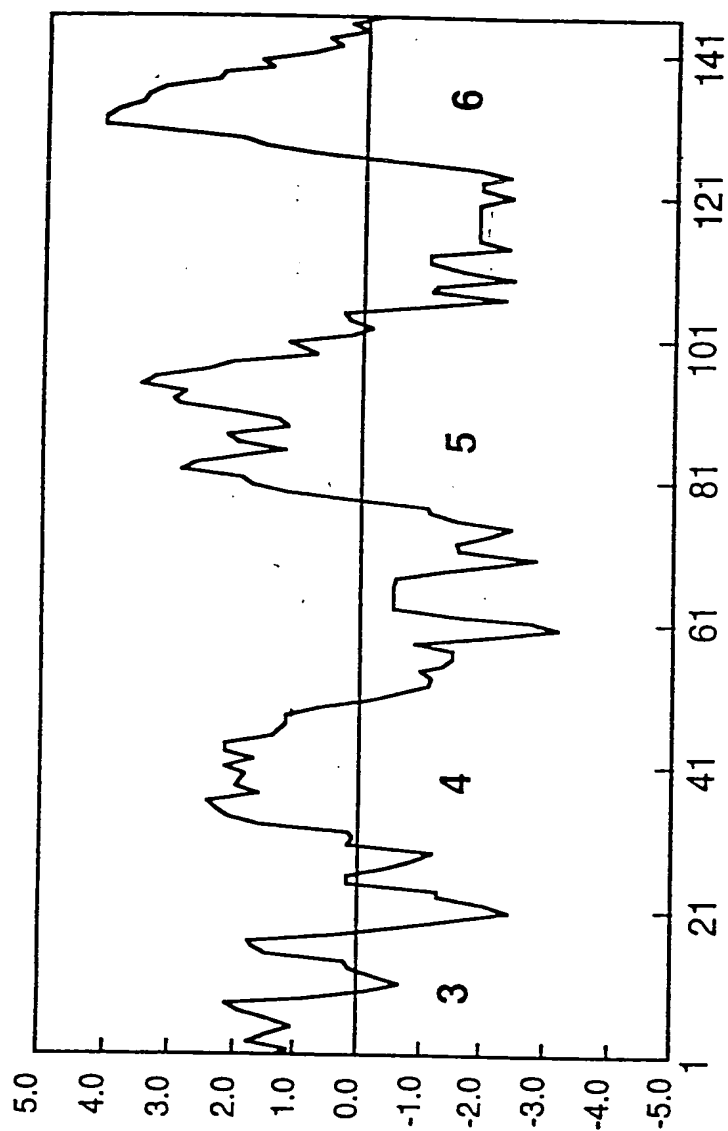
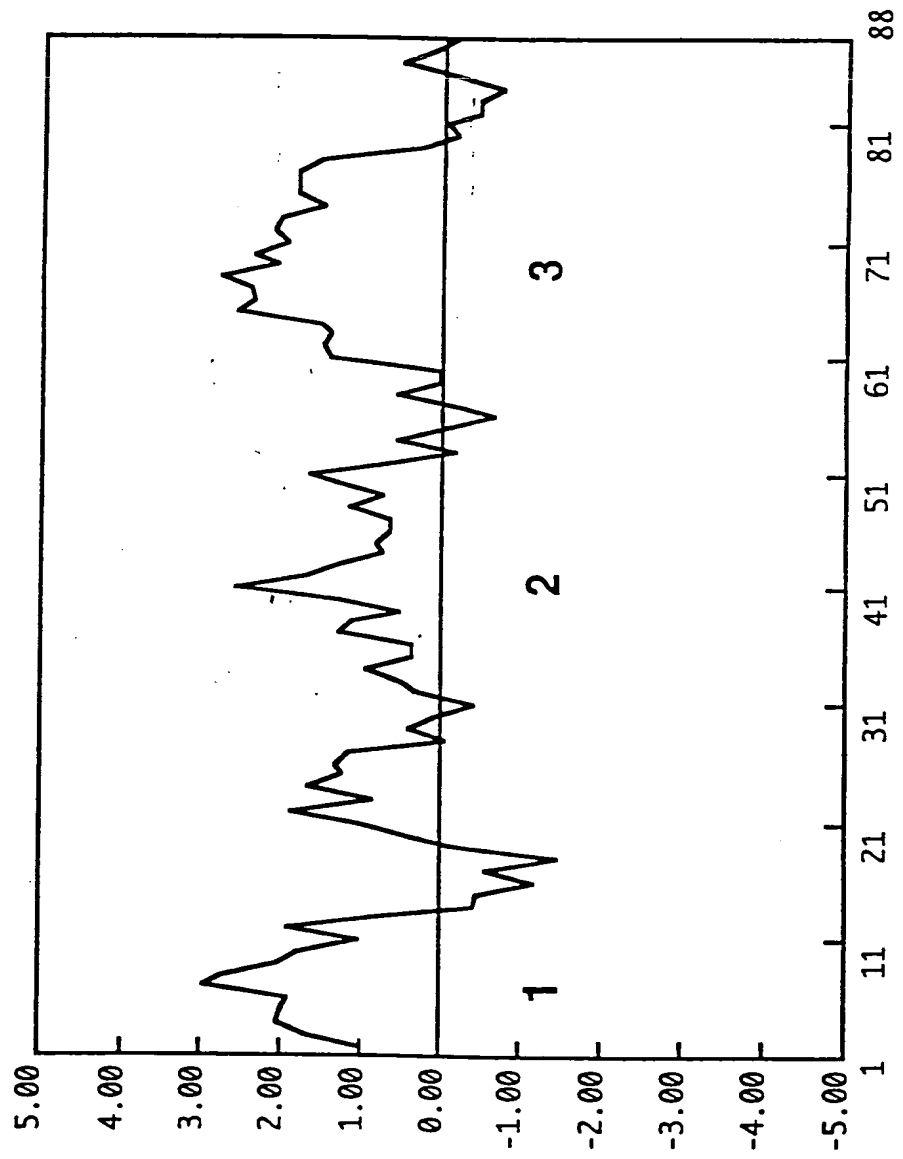


FIGURE 42

p3H2-34	1	VGLVGNF	10	20	30	40	50	50
JN0605	1	MEPSVEGHHV	10	20	30	40	50	50
B41795	1	QFTSTFEGHHV	10	20	30	40	50	50
A39297	1	MEPSIVCHHV	10	20	30	40	50	50
p3H2-34	51	PVA-YHORLF	60	70	80	90	100	100
JN0605	51	PIAIFADTRP	60	70	80	90	100	100
B41795	51	PIMLVAGLRS	60	70	80	90	100	100
A39297	51	PIVVFSTRFA	60	70	80	90	100	100
p3H2-34	101	CFQY----	110	120	130	140	150	150
JN0605	101	GLGYLTLNGK	110	120	130	140	150	150
B41795	101	GLGYLTLNGK	110	120	130	140	150	150
A39297	101	GLGYLTLNGK	110	120	130	140	150	150
p3H2-34	151	FV.....	160	170	180	190	200	200
JN0605	151	FV.....	160	170	180	190	200	200
B41795	151	FV.....	160	170	180	190	200	200
A39297	151	FV.....	160	170	180	190	200	200

	10	19	28	37	46	55
5' GTG GGC ATG GTG GGC AAC GTC CTG GTG CTC TGG TTC TTC GGC TTC TCC ATC AAG						
Val Gly Met Val Gly Asn Val Leu Val Leu Trp Phe Phe Gly Phe Ser Ile Lys						
	64	73	82	91	100	109
AGG ACC CCC TTC TCC TAC TTC CTG CAC CTG GCC AGC GGC GAC GGC GCC TAC						
Arg Thr Pro Phe Ser Val Tyr Phe Leu His Leu Ala Ser Ala Asp Gly Ala Tyr						
	118	127	136	145	154	163
CTC TTC AGC AAG GGC GTG TTC TCC CTG CTG AAC GCC GGC GGC TTC CTG GGC ACC						
Leu Phe Ser Lys Ala Val Phe Ser Leu Leu Asn Ala Gly Gly Phe Leu Gly Thr						
	172	181	190	199	208	217
TTC GCC CAC TAT GTG CGC AGC GTG GCC CGG GTG CTG GCG CTC TGC GCC TTC GTG						
Phe Ala His Tyr Val Arg Ser Val Ala Arg Val Leu Gly Leu Cys Ala Phe Val						
	226	235	244	253	262	
GCG GGC GTG AGC CTC CTG CCG GCC GGC GTG AGC ATG GAG CGC TGC GCG TCT G 3'						
Ala Gly Val Ser Leu Leu Pro Ala Val Ser Met Glu Arg Cys Ala Ser						

[illegible]

pMD4	1	10	20	30	40	50
	1	VGWVGNVLVL	WFFGFSTIKRT	PFSVYFLHLA	SADGAYLFPSK	AVFSLLNAGG
A35639	1	CGLVGNGLVL	WFFGFSTIKRT	PFSIYFLHLA	SADGIYLFPSK	AVIALLENMGT
pMD4	51	60	70	80	90	100
	51	FLGTEAHYVR	SVARVLGLCA	FVAGVSLTLP	VSMERCA	S.....
A35639	51	FLGSEPDYVR	RVSRIVGLCT	FFAGVSLTLP	ISIERCVS

FIGURE 46

1	CAAAGCAACAGGTGCAACCTCAAGGCACTGAAAGCAAGGGGACGAGCTCACAAGGGCCAAGGGATTGAACC	72
1		1
73	CATAACCGCTCAGAAGATTCTCCGCTGCGGAGAGCTGCGGAGGAGTCCCACCCGTCAGCTTGCTGACTGC	144
1		1
145	GAGCAGTGAGAGTGGCCTAGACCCGTACCTCTGTGTTCTGGAGCCTGCCGCCCCCGCACGGGAAAGGCTTAG	216
1		1
217	CTCGGGACTTGCAGCACCGCCTCTCTTTAGCCAGGCCAGGCACGAGGATAGTGTGATCGGGCACAGCCAGG	288
1		1
289	GTGCTCTTCCAGGCTTCTTTCGGGGTTGCGGGAGGTACTAGTTGGAGACGCGCGCTCGCTCTCGCCGCT	360
1		1
361	CTGTCTTGGGCCACTCCGTGATCCTAGGCTACCTCCAGAGCCAGTTTTCCCTGGCTGGCACAACCTCTCCAGG	432
1		1
433	GCGCTCCGGTCCGTTGCACAGCGCCCCAAGGGGGTATCCCAAGTAAGTGATGGAACCTGGCTATGGTGAACCTC	504
1	MetGluLeuAlaMetValAsnLeu	8
505	AGTGAAGGAATGGGAGCGACCCAGAGCCGCCAGCCCCGAGTCCAGGCCGCTCTTCGGCATTGGCGTGGAG	576
8	SerGluGlyAsnGlySerAspProGluProProAlaProGluSerArgProLeuPheGlyIleGlyValGlu	32
577	AACTTCATTACGCTGGTAGTGTTCGGCCTGATTTTCGCGATGGGCGTGCTGGGCAACAGCCTGGTGATCACC	648
32	AsnPheIleThrLeuValValPheGlyLeuIlePheAlaMetGlyValLeuGlyAsnSerLeuValIleThr	56
649	GTGCTGGCGCGCAGCAAACAGGCAAGCCGCGCAGCACCACCAACCTGTTTATCCTCAATCTGAGCATCGCA	720
56	ValLeuAlaArgSerLysProGlyLysProArgSerThrThrAsnLeuPheIleLeuAsnLeuSerIleAla	80
721	GACCTGGCCTACCTGCTCTTCTGCATCCCTTTTCAGGCCACCGTGTATGCACTGCCACCTGGGTGCTGGGC	792
80	AspLeuAlaTyrLeuLeuPheCysIleProPheGlnAlaThrValTyrAlaLeuProThrTrpValLeuGly	104
793	GCCTTCATCTGCAAGTTTATACACTACTTCTTCACCGTGTCCATGCTGGTGAGCATCTTCACCCTGGCCGCG	864
104	AlaPheIleCysLysPheIleHisTyrPhePheThrValSerMetLeuValSerIlePheThrLeuAlaAla	128
865	ATGTCTGTGGATCGCTACGTGGCCATTGTGCACTCGCGCGCTCCTCCTCCCTCAGGGTGTCCCGCAACGCA	936
128	MetSerValAspArgTyrValAlaIleValHisSerArgSerSerLeuArgValSerArgAsnAla	152
937	CTGCTGGGCGTGGGCTTCATCTGGGCGCTGTCTATCGCCATGGCCTCGCCGGTGGCCTACCACCAGCGTCTT	1008
152	LeuLeuGlyValGlyPheIleTrpAlaLeuSerIleAlaMetAlaSerProValAlaTyrHisGlnArgLeu	176
1009	TTCCATCGGGACAGCAACCAAGACCTTCTGCTGGGAGCAGTGGCCCCAACAAGCTCCACAAGAAGGCTTACGTG	1080
176	PheHisArgAspSerAsnGlnThrPheCysTrpGluGlnTrpProAsnLysLeuHisLysLysAlaTyrVal	200
1081	GTGTGCACTTTCGTCTTTGGGTACCTTCTGCCCTTACTGCTCATCTGCTTTTGCTATGCCAAGGTCCTTAAT	1152
200	ValCysThrPheValPheGlyTyrLeuLeuProLeuLeuLeuIleCysPheCysTyrAlaLysValLeuAsn	224
1153	CATCTGCATAAAAAGCTGAAAAACATGTCAAAAAGTCTGAAGCATCCAAGAAAAAGACTGCACAGACCGTC	1224
224	HisLeuHisLysLysLeuLysAsnMetSerLysLysSerGluAlaSerLysLysLysThrAlaGlnThrVal	248
1225	CTGGTGGTCTGTGTAGTATTTGGCATATCCTGGCTGCCCCATCATGCTGCTCCACCTCTGGGCTGAGTTTGGGA	1296
248	LeuValValValValValPheGlyIleSerTrpLeuProHisHisValValHisLeuTrpAlaGluPheGly	272
1297	GCCTTCCCCTGACGCCAGCTTCTCTTCTTCTCAGAATCACCGCCCATGCTGGCATAACAGCAACTCCTCA	1368
272	AlaPheProLeuThrProAlaSerPhePhePheArgIleThrAlaHisCysLeuAlaTyrSerAsnSerSer	296
1369	GTGAACCCCATCATATATGCCTTTCTCTCAGAAAACCTTCGGAAGGCGTACAAGCAAGTGTTCAGTGTTCAT	1440
296	ValAsnProIleIleTyrAlaPheLeuSerGluAsnPheArgLysAlaTyrLysGlnValPheLysCysHis	320
1441	GTTTGCATGAATCTCCACGCAGTGAAGTAAAGGAAAACAAGAGCCGGATGGACACCCCGCCATCCACCAAC	1512
320	ValCysAspGluSerProArgSerGluThrLysGluAsnLysSerArgMetAspThrProProSerThrAsn	344
1513	TGCACCCACGTGTGAAGGTTTTCGGGAGCCTCCCGACTTCCAGCTCCCATGTGTGTAGAGAGAGGAGGGCG	1584
344	CysThrHisVal***	349
1585	GAGCGAATTATCAAGTAACATGG	1607
349		349

FIGURE 47

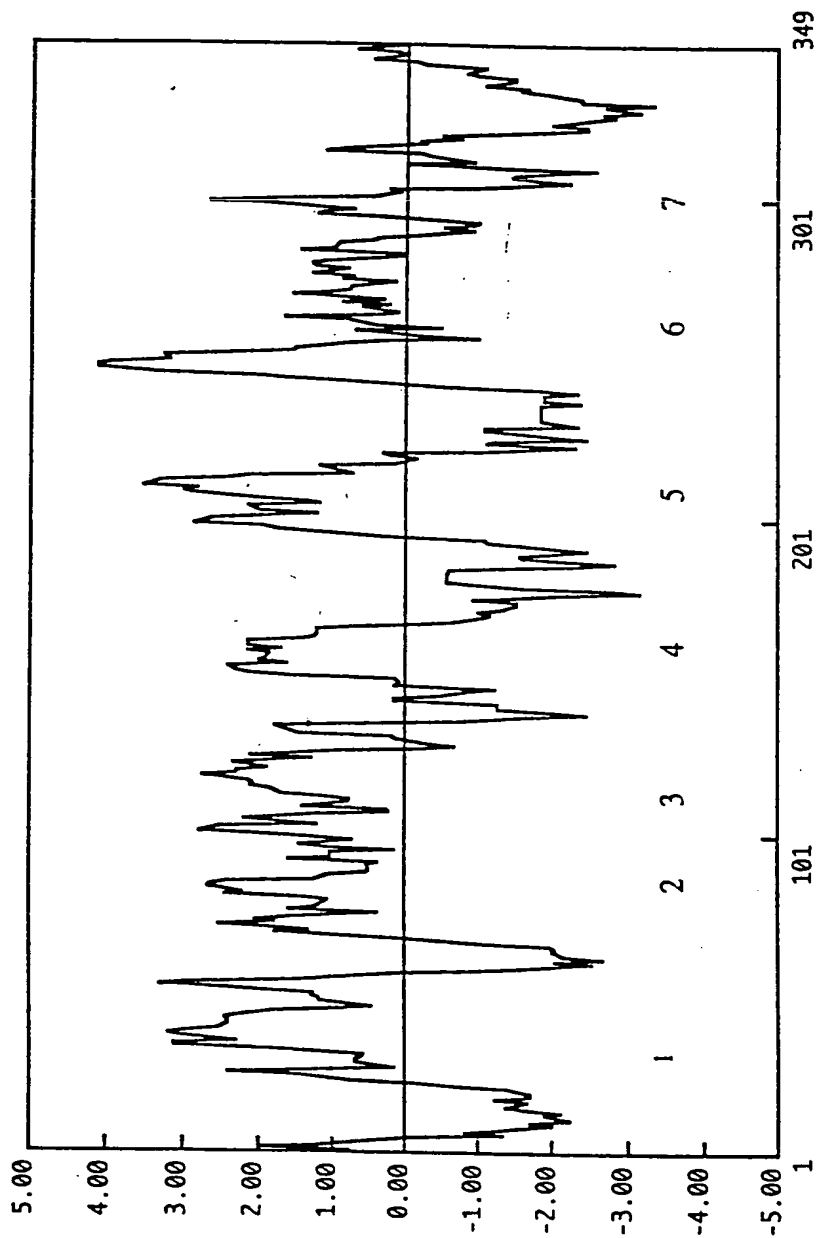


FIGURE 48

MOUSEGALRECE	1	10	20	30	40	50	
HUMGALAMI	1	MELAVNASE	GNSSDPEPPA	PESSRPLEFGIG	VENFTITAVVF	QIFAVGVFG	50
	1	MELAVNISE	GNASCPPEPPA	PEEGPLEFGIG	VENFTITAVVF	GLIFALGVLC	50
MOUSEGALRECE	51	60	70	80	90	100	
HUMGALAMI	51	NSLAVITVLEAR	SKPGKPRSTT	NLFILNLSIA	DHAYLLEFCIP	EQATVVALPT	100
	51	NSLAVITVLEAR	SKPGKPRSTT	NLFILNLSIA	DHAYLLEFCIP	EQATVVALPT	100
MOUSEGALRECE	101	110	120	130	140	150	
HUMGALAMI	101	WVLGAFICKF	IHYFFFTVSM	VSIFTLAAMS	VDRYVALVHS	RRSSSLRVS	150
	101	WVLGAFICKF	IHYFFFTVSM	VSIFTLAAMS	VDRYVALVHS	RRSSSLRVS	150
MOUSEGALRECE	151	160	170	180	190	200	
HUMGALAMI	151	NALLGVGFIM	ALSTAVASPV	AYHORLEH-R	DSNOTFCWEQ	WPNKLHKAY	200
	151	NALLGVGFIM	ALSTAVASPV	AYHOSLEHPR	ASNOTFCWEQ	WPDPRHKAY	200
MOUSEGALRECE	201	210	220	230	240	250	
HUMGALAMI	201	WCTFVEGYL	LPLILITFCY	AKVANHLHKK	LKNVSKKSEA	SKKKYACTVL	250
	201	WCTFVEGYL	LPLILITFCY	AKVANHLHKK	LKNVSKKSEA	SKKKYACTVL	250
MOUSEGALRECE	251	260	270	280	290	300	
HUMGALAMI	251	VVVVVEGISM	LRPHVHLWA	BECAFRLTPA	SFFERITAH	LAYSNSVNP	300
	251	VVVVVEGISM	LRPHVHLWA	BECAFRLTPA	SFFERITAH	LAYSNSVNP	300
MOUSEGALRECE	301	310	320	330	340	350	
HUMGALAMI	301	LIYAFLESEF	RKAYKQVFKC	HVCDESPRSE	TKENKSRVDT	PPSTNCTHAX	350
	301	LIYAFLESEF	RKAYKQVFKC	HVKDSEILSD	TKENKSRVDT	PPSTNCTHAX	350
MOUSEGALRECE	351	360	370	380	390	400	
HUMGALAMI	351	400
	351	X.....	400

FIGURE 49

5'	CTC	GCG	GCT	CTG	GGT	ATG	GAT	CGG	TAT	CTT	CTC	ACC	CTT	CAC	CCA	GTG	TGG	TCC	
										Leu	Leu	Thr	Leu	His	Pro	Val	Trp	Ser	
	CAA	AAG	CAC	CGA	ACC	TCA	CAC	TGG	GCT	TCC	AGA	GTC	GTT	CTG	GGA	GTC	TGG	CTC	108
	Gln	Lys	His	Arg	Thr	Ser	His	Trp	Ala	Ser	Arg	Val	Val	Leu	Gly	Val	Trp	Leu	
	TCT	GCC	ACT	GCC	TTC	AGC	GTG	CCC	TAT	TTG	GTT	TTC	AGG	GAG	ACA	TAT	GAT	GAC	162
	Ser	Ala	Thr	Ala	Phe	Ser	Val	Pro	Tyr	Leu	Val	Phe	Arg	Glu	Thr	Tyr	Asp	Asp	
	CGT	AAA	GGA	AGA	GTG	ACC	TGC	AGA	AAT	AAC	TAC	GCT	GTG	TCC	ACT	GAC	TGG	GAA	216
	Arg	Lys	Gly	Arg	Val	Thr	Cys	Arg	Asn	Asn	Tyr	Ala	Val	Ser	Thr	Asp	Trp	Glu	
	AGC	AAA	GAG	ATG	CAA	ACA	GTA	AGA	CAA	TGG	ATT	CAT	GCC	ACC	TGT	TTC	ATC	AGC	270
	Ser	Lys	Glu	Met	Gln	Thr	Val	Arg	Gln	Trp	Ile	His	Ala	Thr	Cys	Phe	Ile	Ser	
	CGC	TTC	ATA	CTG	GGC	TTC	CTT	CTG	CCT	TTC	TTA	GTC	ATT	GGC	TTT	TGT	TAT	GAA	324
	Arg	Phe	Ile	Leu	Gly	Phe	Leu	Leu	Pro	Phe	Leu	Val	Ile	Gly	Phe	Cys	Tyr	Glu	
	AGA	GTA	GCC	CGC	AAG	ATG	AAA	GAG	AGG	GGC	CTC	TTT	AAA	TCC	AGC	AAA	CCC	TTC	378
	Arg	Val	Ala	Arg	Lys	Met	Lys	Glu	Arg	Gly	Leu	Phe	Lys	Ser	Ser	Lys	Pro	Phe	
	AAA	GTC	ACG	ATG	ACT	GCT	GTT	ATC	TCT	TTT	TTC	TGT	CCT	GGC	TTC	CCT	ACC	ACA	432
	Lys	Val	Thr	Met	Thr	Ala	Val	Ile											

TG 3'

FIGURE 50

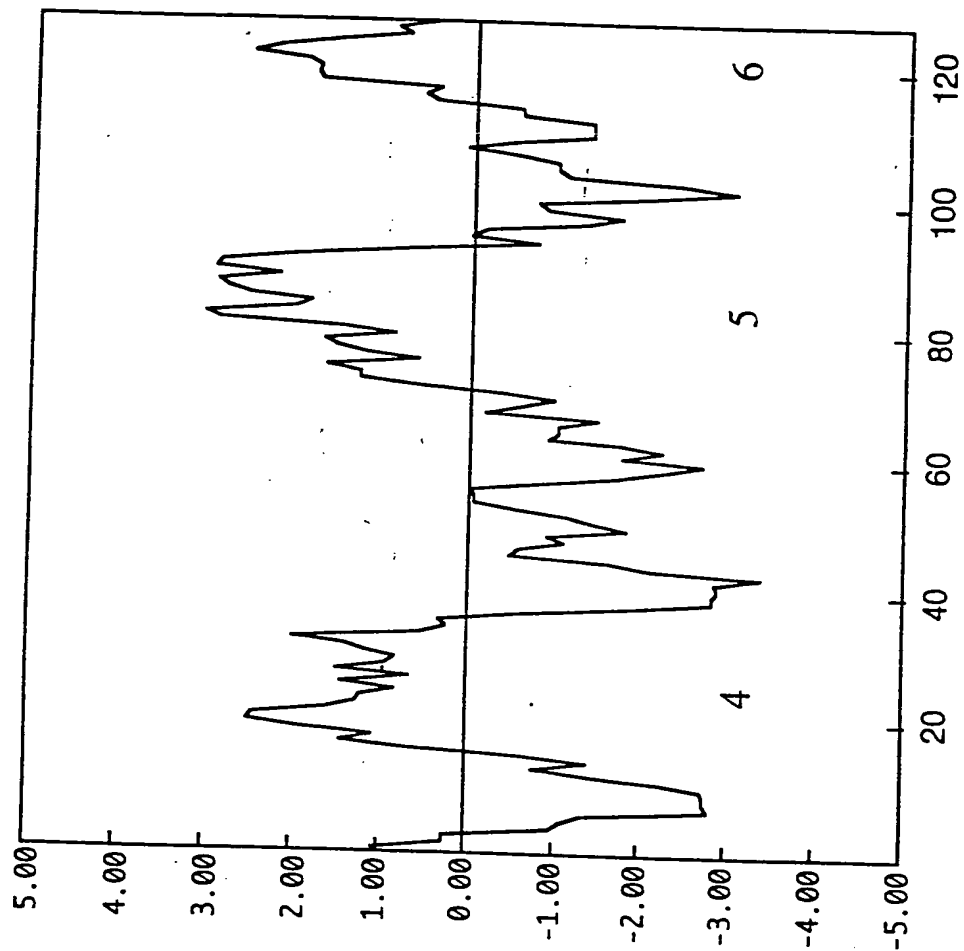


FIGURE 51

pmj10	1	10	20	30	40	50	50
B42009	1	1	1	1	1	1	50
JC2014	1	1	1	1	1	1	50
A46520	1	1	1	1	1	1	50
A46525	1	1	1	1	1	1	50
S28787	1	1	1	1	1	1	50
pmj10	51	60	70	80	90	100	100
B42009	51	51	51	51	51	51	100
JC2014	51	51	51	51	51	51	100
A46520	51	51	51	51	51	51	100
A46525	51	51	51	51	51	51	100
S28787	51	51	51	51	51	51	100
pmj10	101	110	120	130	140	150	150
B42009	101	101	101	101	101	101	150
JC2014	101	101	101	101	101	101	150
A46520	101	101	101	101	101	101	150
A46525	101	101	101	101	101	101	150
S28787	101	101	101	101	101	101	150

[illegible][illegible]

FIGURE 53

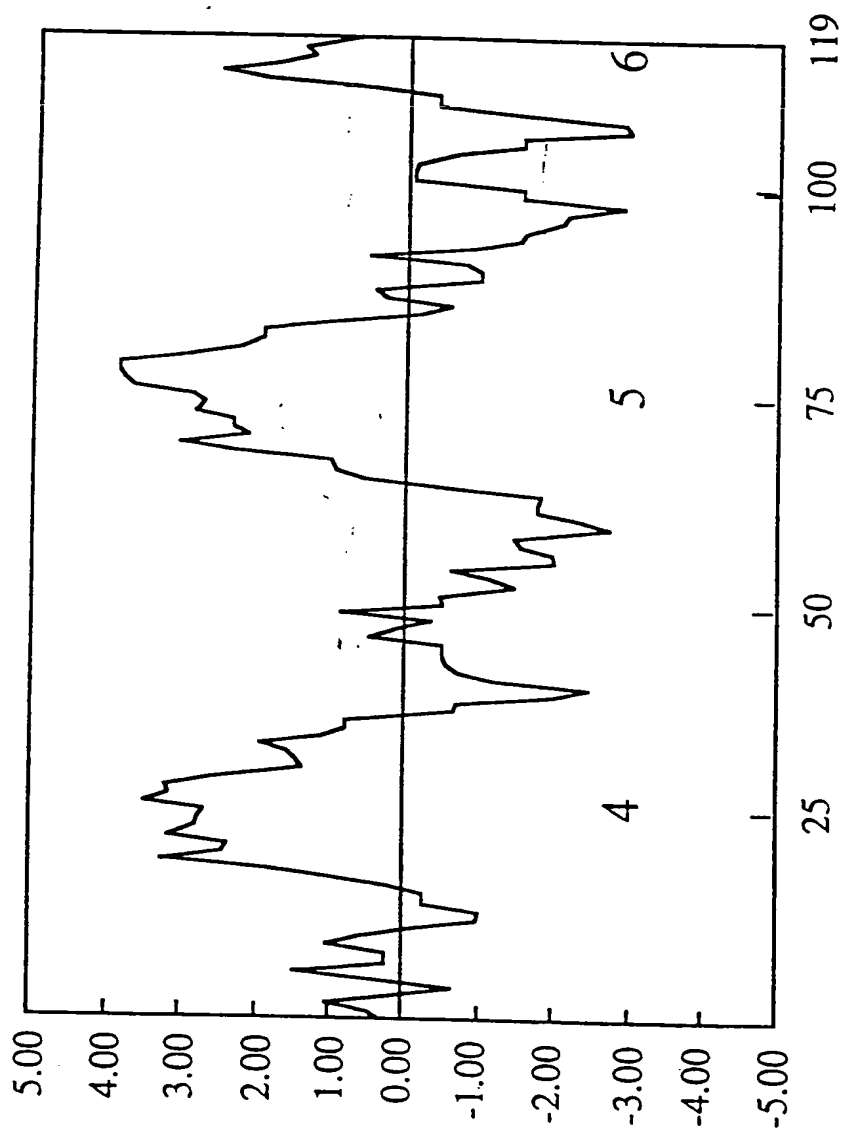


FIGURE 54

pMH28	10	20	30	40	50
P35343	1 FKIVKPLSIS	FIQSVNYSKL	VSLVWMLML	LIAVPNVVLTIT	NQRVKDVTQI
A41795	1 LAIVFATSP-	LIQKRHLVKE	YCIAMMLLESV	IIPALPILITR	NPVKVNLSTL
A47457	1 YAVVHEIKAA	RYRRPTIVAKV	VNHGVWVESL	LVIIPFVWES	RTAANSDDIV
	1 VAVVHPLRAA	TYRRPSVAKL	INLGVNLASL	LVTETRIATFA	DTRPARGGQ-
					50
pMH28	60	70	80	90	100
P35343	51 KOME-LKNEI	GROWHKASNY	IFVGIF-WLV	FLLIILFYTA	IT-RKIFKSH
A41795	51 VCYEEDVGNT	SRL--RVVLR	ILPQTEGFLV	PPLIMLFQYG	FYLRFLFKAH
A47457	51 AQNM-LMPEP	AQRMLVGEV-	LYTFLMGFLI	PVGATCLQV	LITAKVRMVA
	51 AVAC-NLQWF	HPAWSAVFV-	VYTFLLGFLI	PVLEAIGLCYL	LIVGKMRAYA
					100
pMH28	110	120	130	140	150
P35343	101 LKSRKNSI-S	VKKKSSRNIF	S--IV
A41795	101 MG----QKRR	AMR----VIF	AVVLV
A47457	101 EKAGWQQRKR	SERKTLTMVM	MVMV
	101 LRAGWQQRKR	SEKKITRLVL	MVMV
					150

FIGURE 55

	9	18	27	36	45	54												
5'	GCC	ACC	AAC	GTG	TTC	ATC	CTG	TGT	CTG	GTG	GAC	CTG	GCT	GCC	CTG	ACC	CTC	
										Val	Asp	Leu	Leu	Ala	Ala	Leu	Thr	Leu
	63	72	81	90	99	108												
	ATG	CCT	CTG	GCC	ATG	CTC	TCC	AGC	TCC	GCC	CTC	TTT	GAC	CAC	GCC	CTC	TTT	GGG
	Met	Pro	Leu	Ala	Met	Leu	Ser	Ser	Ser	Ala	Leu	Phe	Asp	His	Ala	Leu	Phe	Gly
	117	126	135	144	153	162												
	GAG	GTG	GCC	TGC	CGC	CTC	TAC	TTG	TTC	CTG	AGC	GTC	TGC	TTT	GTC	AGC	CTG	GCC
	Glu	Val	Ala	Cys	Arg	Leu	Tyr	Leu	Phe	Leu	Ser	Val	Cys	Phe	Val	Ser	Leu	Ala
	171	180	189	198	207	216												
	ATC	CTC	TCG	GTG	TCC	GCC	ATC	AAT	GTG	GAG	CGC	TAC	TAT	TAT	GTG	GTC	CAC	CCC
	Ile	Leu	Ser	Val	Ser	Ala	Ile	Asn	Val	Glu	Arg	Tyr	Tyr	Tyr	Val	Val	His	Pro
	225	234	243	252	261	270												
	ATG	CGC	TAT	GAG	GTG	CGC	ATG	AAA	CTG	GGG	CTG	GTG	GCC	TCT	GTG	CTG	GTG	GGC
	Met	Arg	Tyr	Glu	Val	Arg	Met	Lys	Leu	Gly	Leu	Val	Ala	Ser	Val	Leu	Val	Gly
	279	288	297	306	315	324												
	GTG	TGG	GTG	AAG	GCC	CTG	GCC	ATG	GCT	TCT	GTG	CCA	GTG	TTG	GGA	AGG	GTG	TCC
	Val	Trp	Val	Lys	Ala	Leu	Ala	Met	Ala	Ser	Val	Pro	Val	Leu	Gly	Arg	Val	Ser
	333	342	351	360	369	378												
	TGG	GAG	GAA	GGC	CCT	CCC	AGT	GTC	CCC	CCA	GGC	TGT	TCA	CTC	CAA	TGG	AGC	CAC
	Trp	Glu	Glu	Gly	Pro	Pro	Ser	Val	Pro	Pro	Gly	Cys	Ser	Leu	Gln	Trp	Ser	His
	387	396	405	414	423	432												
	AGT	GCC	TAC	TGC	CAG	CTT	TTC	GTG	GTG	GTC	TTC	GCC	GTC	CTC	TAC	TTC	CTG	CTG
	Ser	Ala	Tyr	Cys	Gln	Leu	Phe	Val	Val	Val	Phe	Ala	Val	Leu	Tyr	Phe	Leu	Leu
	441	450	459	468	477	486												
	CCC	CTG	CTC	CTC	ATC	CTT	GTG	GTC	TAC	TGC	AGC	ATG	TTC	CGG	GTG	GCT	CGT	GTG
	Pro	Leu	Leu	Leu	Ile	Leu	Val	Val	Tyr	Cys	Ser	Met	Phe	Arg	Val	Ala	Arg	Val
	495	504	513	522	531	540												
	GCT	GCC	ATG	CAG	CAC	GGG	CCG	CTG	CCC	ACG	TGG	ATG	GAG	ACG	CCC	CGG	CAA	CGC
	Ala	Ala	Met	Gln	His	Gly	Pro	Leu	Pro	Thr	Trp	Met	Glu	Thr	Pro	Arg	Gln	Arg

FIGURE 56

549	558	567	576	585	594
TCC GAG TCT CTC AGC	AGC CGC TCC ACT	ATG GTC ACC AGC	TCG GGG GCC CCG	CAG	
---	---	---	---	---	---
Ser Glu Ser Leu Ser	Ser Arg Ser Thr Met	Val Thr Ser Ser	Gly Ala Pro	Gln	
603	612	621	630	639	648
ACC ACC CCT CAC CGG	ACG TTT GGC GGA	GGG AAG GCA GCA	GTG GTC CTC CTG	GCT	
---	---	---	---	---	---
Thr Thr Pro His Arg	Thr Phe Gly Gly	Gly Lys Ala Ala	Val Val Leu Leu	Ala	
657	666	675	684	693	702
GTG GGA GGA CAG TTC	CTG CTC TGT TGG	TTG CCC TAC TTC	TCC TTC CAC CTC	TAT	
---	---	---	---	---	---
Val Gly Gly Gln Phe	Leu Leu Cys Trp	Leu Pro Tyr Phe	Ser Phe His Leu	Tyr	
711	720	729	738	747	756
GTG GCC CTG AGC GCT	CAG CCC ATT GCA	GCG GGG CAG GTG	GAG AAC GTG GTG	ACC	
---	---	---	---	---	---
Val Ala Leu Ser Ala	Gln Pro Ile Ala	Ala Gly Gln Val	Glu Asn Val Val	Thr	
765	774	783	792	801	810
TGG ATT GGC TAC TTC	TGC TTC ACC TCC	<u>AAC CCT CTC CTC TAT</u>	<u>TCC TTC CTC CCT</u>	3'	
---	---	---	---	---	---
Trp Ile Gly Tyr Phe	Cys Phe Thr Ser				

FIGURE 57

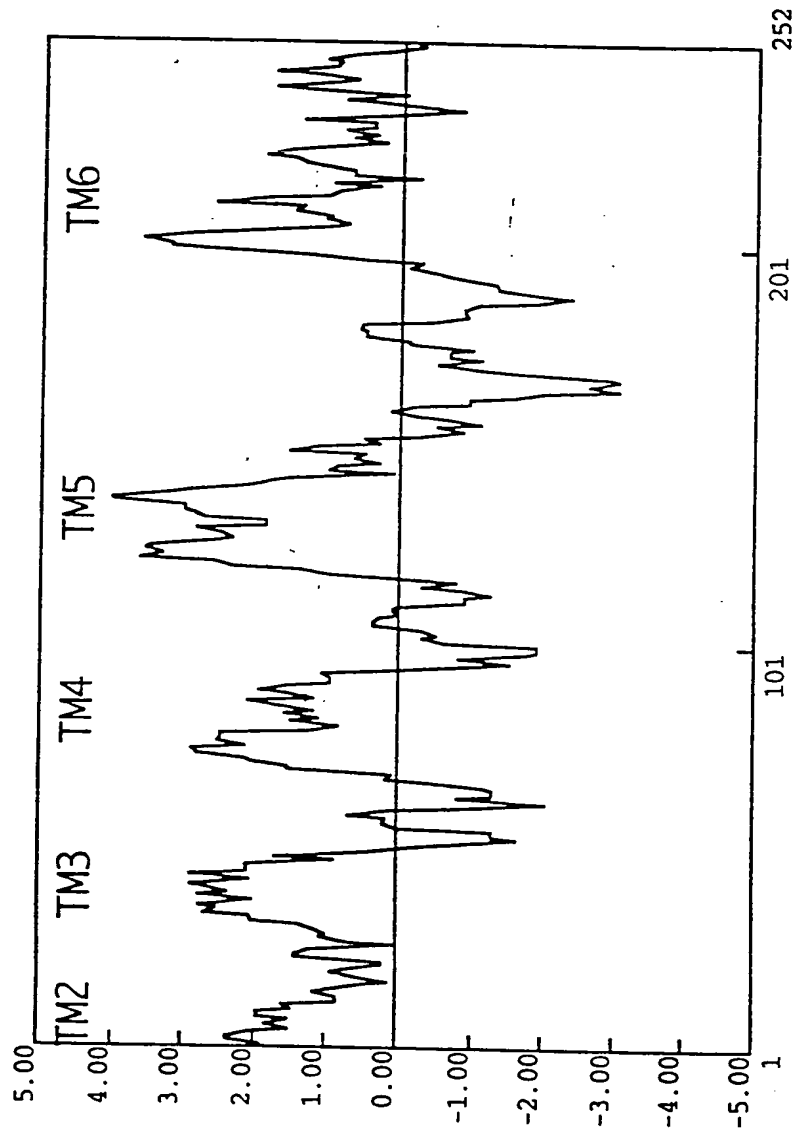


FIGURE 58

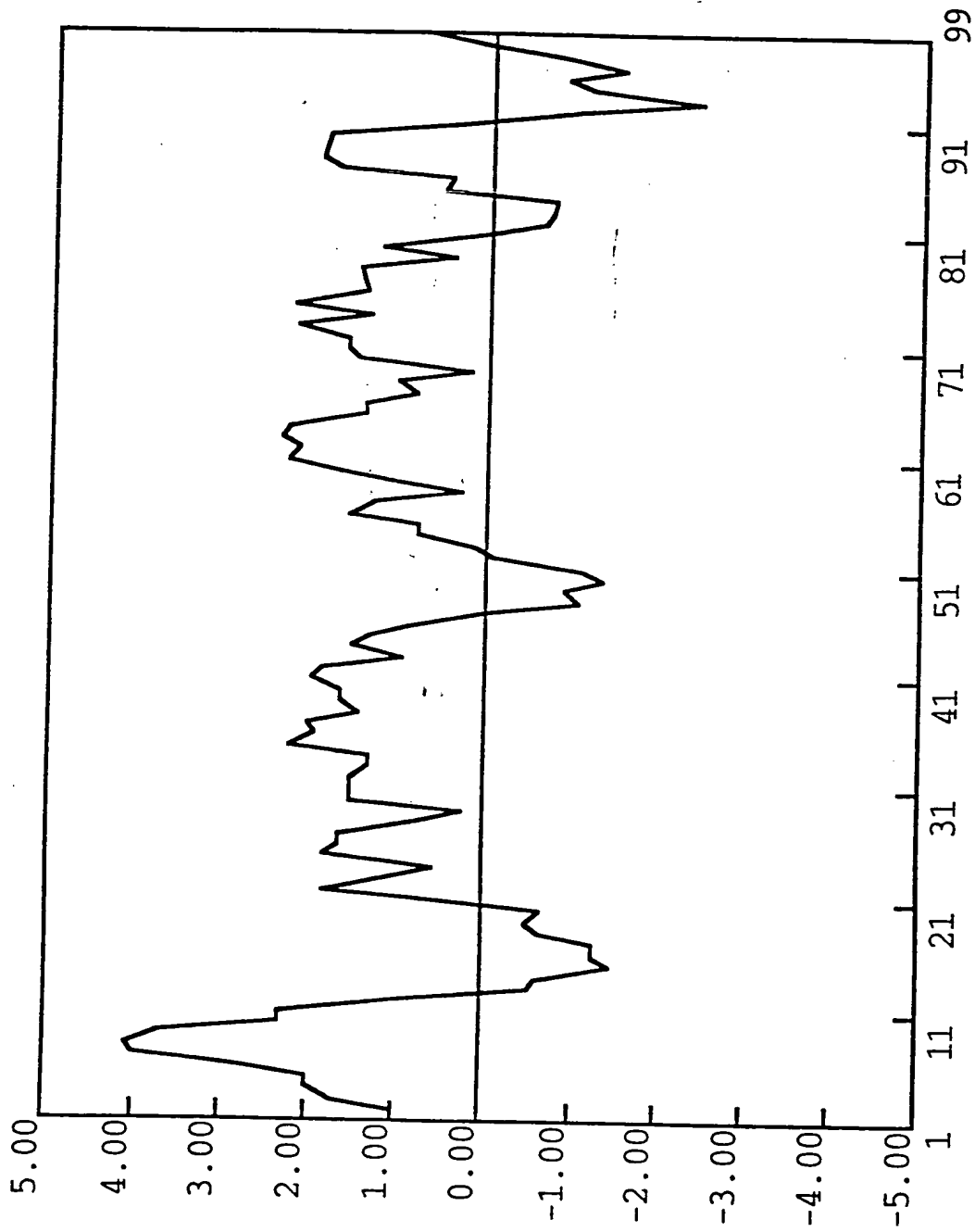


FIGURE 59

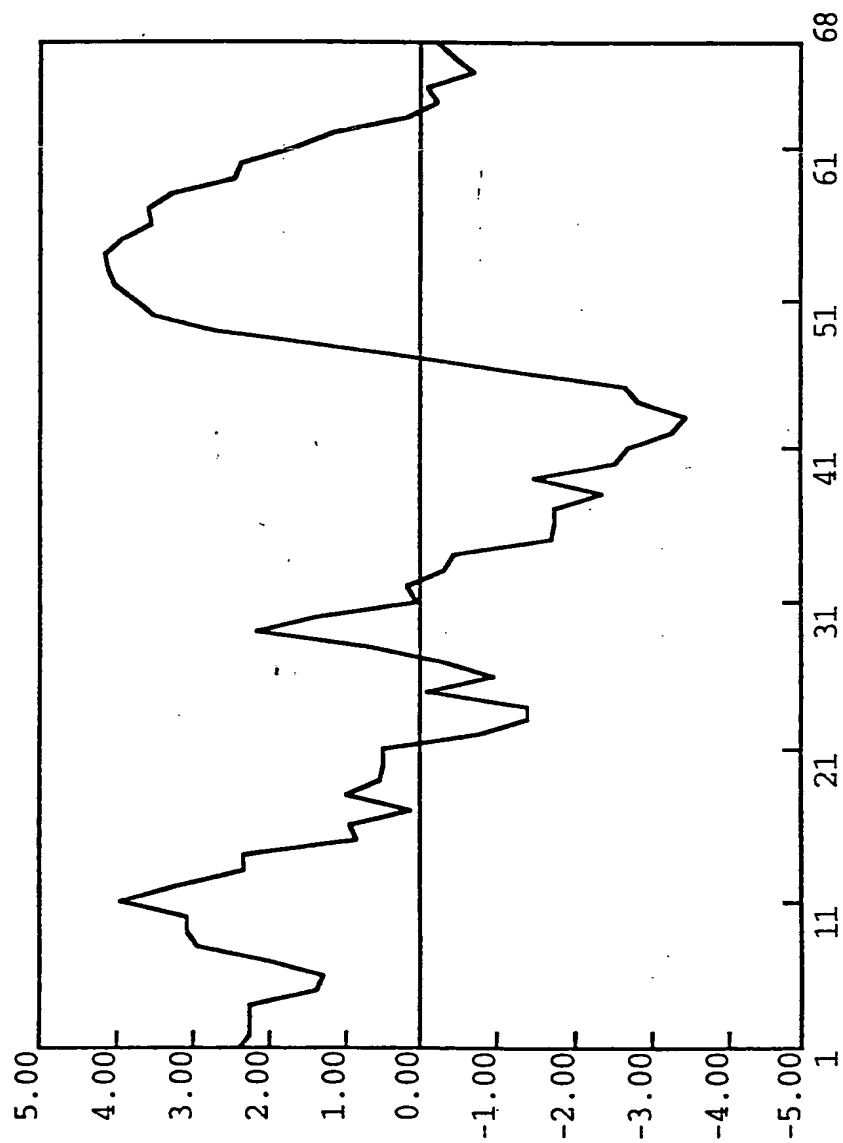


FIGURE 60

p19P2	1	10	20	30	40	50	
S12863	1	VGVMGNVLIV	LVIAVRRLH	NVTNFIIGNL	ALSDVLMCTA	CVPLTLAVAF	50
	1	LGVSGLALAI	IIILKQEMR	NVTNFIIGNL	SFSDLLAVAM	CLPFTFVYIL	50
p19P2	51	60	70	80	90	100	
S12863	51	EPRGMVEGGG	LCHLVFLQIP	VIVYVSFTIL	TTIAVDRYV	LVHPLRRRI-	100
	51	MDH-WVEGET	MCKLNPVQ	VSITVSIEST	VLIAVERHQL	IINPRGWRPN	100
p19P2	101	110	120	130	140	150	
S12863	101	NRHAYIGITV	IWVLAVASSL	PFVIYQILTD	EPFQNVSLAA	FKDKYVCFDK	150
p19P2	151	160	170	180	190	200	
S12863	151	-----GLLV	TYLPLLVIL	LS-----Y	VRVSVKLRNR	VVPGCVTQSQ	200
	151	FPSDSHRLSY	TIPLLVVQYF	GPLCFIFICY	FKIYIRLKR	NNMMDKIRDS	200
p19P2	201	210	220	230	240	250	
S12863	201	ADWDRARRRR	TFCLLVVVW	VFAICWLEFY	250
	201	KVRSSETKRI	NVMELISIVA	-FAVCWLEPLT	250

[illegible]

FIGURE 62

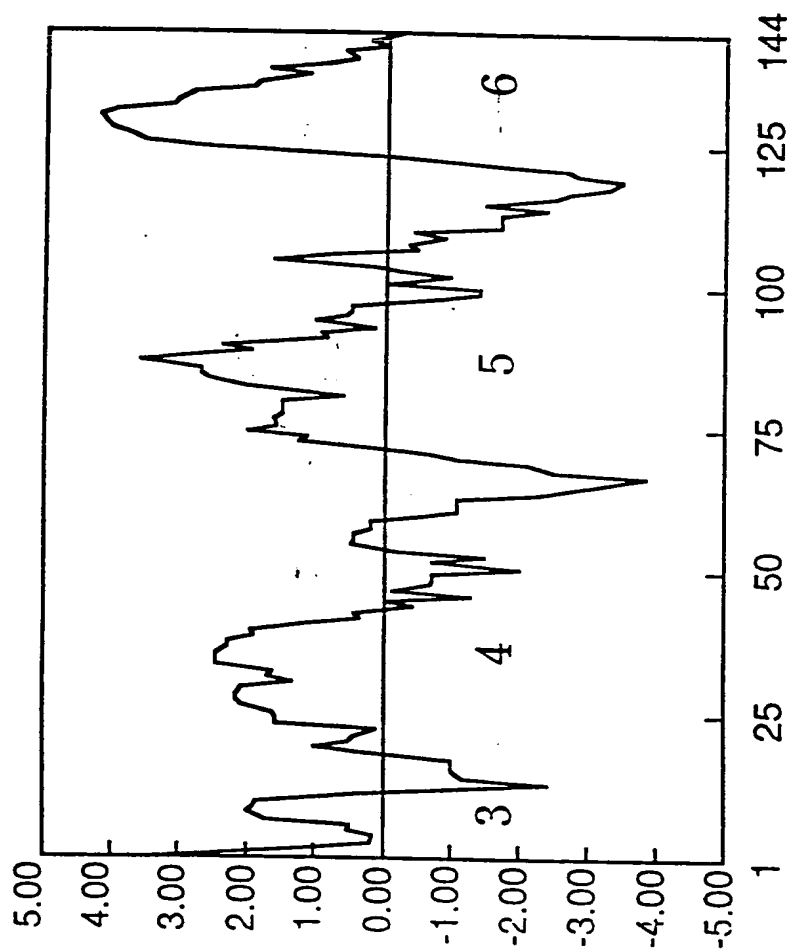
5'	CTG	TGT	9	ATC	GCG	18	GTG	GAT	27	AGG	TAC	GTG	GTT	36	CTG	GTG	CAC	45	CCG	CTA	CGT	54	CGG
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Leu	Cys	Val	Ile	Ala	Val	Asp	Arg	Tyr	Val	Val	Leu	Val	His	Pro	Leu	Arg	Arg	Arg	Arg	Arg	Arg	Arg
	63	63	63	63	63	63	63	63	63	63	63	63	63	63	63	63	63	63	63	63	63	63	63
	CGC	ATT	TCA	CTG	AGG	CTC	AGC	GCC	TAC	GCG	GTG	CTG	GGC	ATC	TGG	GCT	CTA	TCT	TCT	TCT	TCT	TCT	TCT
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Arg	Ile	Ser	Leu	Arg	Leu	Ser	Ala	Tyr	Ala	Val	Leu	Gly	Ile	Trp	Ala	Leu	Ser	Ser	Ser	Ser	Ser	Ser
	117	117	117	117	117	117	117	117	117	117	117	117	117	117	117	117	117	117	117	117	117	117	117
	GCA	GTG	CTG	GCG	CTG	CCG	GCC	GCG	GTG	CAC	ACC	TAC	CAT	GTG	GAG	CTC	AAG	CCC	CCC	CCC	CCC	CCC	CCC
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Ala	Val	Leu	Ala	Leu	Pro	Ala	Ala	Val	His	Thr	Tyr	His	Val	Glu	Leu	Lys	Pro	Pro	Pro	Pro	Pro	Pro
	171	171	171	171	171	171	171	171	171	171	171	171	171	171	171	171	171	171	171	171	171	171	171
	CAC	GAC	GTG	AGC	CTC	TGC	GAG	GAG	TTC	TGG	GGC	TCG	CAG	GAG	CGC	CAA	CGC	CAG	CAG	CAG	CAG	CAG	CAG
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	His	Asp	Val	Ser	Leu	Cys	Glu	Glu	Phe	Trp	Gly	Ser	Gln	Glu	Arg	Gln	Arg	Gln	Gln	Gln	Gln	Gln	Gln
	225	225	225	225	225	225	225	225	225	225	225	225	225	225	225	225	225	225	225	225	225	225	225
	ATC	TAC	GCC	TGG	GGG	CTG	CTT	CTG	GGC	ACC	TAT	TTG	CTC	CCC	CTG	CTG	GCC	ATC	ATC	ATC	ATC	ATC	ATC
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Ile	Tyr	Ala	Trp	Gly	Leu	Leu	Leu	Gly	Thr	Tyr	Leu	Leu	Pro	Leu	Leu	Ala	Ile	Ile	Ile	Ile	Ile	Ile
	279	279	279	279	279	279	279	279	279	279	279	279	279	279	279	279	279	279	279	279	279	279	279
	CTC	CTG	TCT	TAC	GTA	CGG	GTG	TCA	GTG	AAG	CTG	AGG	AAC	CGC	GTG	GTG	CCT	GGC	GGC	GGC	GGC	GGC	GGC
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Leu	Leu	Ser	Tyr	Val	Arg	Val	Ser	Val	Lys	Leu	Arg	Asn	Arg	Val	Val	Pro	Gly	Gly	Gly	Gly	Gly	Gly
	333	333	333	333	333	333	333	333	333	333	333	333	333	333	333	333	333	333	333	333	333	333	333
	AGC	GTG	ACC	CAG	AGT	CAA	GCT	GAC	TGG	GAC	CGA	GCG	CGT	CGC	CGC	CGC	ACT	TTC	TTC	TTC	TTC	TTC	TTC
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Ser	Val	Thr	Gln	Ser	Gln	Ala	Asp	Trp	Asp	Arg	Ala	Arg	Arg	Arg	Arg	Thr	Phe	Phe	Phe	Phe	Phe	Phe
	387	387	387	387	387	387	387	387	387	387	387	387	387	387	387	387	387	387	387	387	387	387	387
	TGT	CTG	CTG	GTG	GTG	GTG	GTG	GTA	GTG	TTC	ACG	CTC	TGC	TGG	423	CTG	CCC	TTC	TAC	TAC	TAC	TAC	TAC
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Cys	Leu	Leu	Val	Val	Val	Val	Val	Val	Phe	Thr	Leu	Cys	Trp	Leu	Pro	Phe	Tyr	Tyr	Tyr	Tyr	Tyr	Tyr

CT 3'

FIGURE 63

p19P2	1	10	20	30	40	50	
pg3-2/pg1-10	1	VGMVGNLLV	LVIAVRRLH	NVINEELIGN	ALSDVLMGTA	CVPLTLAYAF	50
p5S38	-79	VGMVGNLLV	LVIAVRRLV	NVINEELIGN	ALSDVLMGTA	CVPLTLAYAF	50
							-30
p19P2	51	60	70	80	90	100	
pg3-2/pg1-10	51	EPRGMVFGGG	LCHLVFELOP	VTVVSVSETL	TTTAVDRVAV	LVHPLRRRI	100
p5S38	-29	EPRGMVFGGG	LCHLVFELOA	VTVVSVSETL	TTTAVDRVAV	LVHPLRRRI	100
					CVIAVDRVAV	LVHPLRRRI	21
p19P2	101	110	120	130	140	150	
pg3-2/pg1-10	101	LRLSAYAVLA	HWLSAVTAL	PAAVHTYHVE	LKPHDVRLCE	EFMGSQERQR	150
p5S38	22	LRLSAYAVLG	HWLSAVTAL	PAAVHTYHVE	LKPHDVRLCE	EFMGSQERQR	150
							71
p19P2	151	160	170	180	190	200	
pg3-2/pg1-10	151	QLYANGLLLV	TYLLPLLVIL	LSYVRVSVKL	RNRVAVPGCVT	QSQADMDDRAR	200
p5S38	72	QLYANGLLLG	TYLLPLLVIL	LSYVRVSVKL	RNRVAVPGCVT	QSQADMDDRAR	200
					RNRVAVPGCVT	QSQADMDDRAR	121
p19P2	201	210	220	230	240	250	
pg3-2/pg1-10	201	RRRTFCLLVV	VVVVFAICWL	PYY			250
p5S38	122	RRRTFCLLVV	VVVVFTLCWL	PFF			250
							171

FIGURE 64



6 5 / 7 9

FIGURE 65

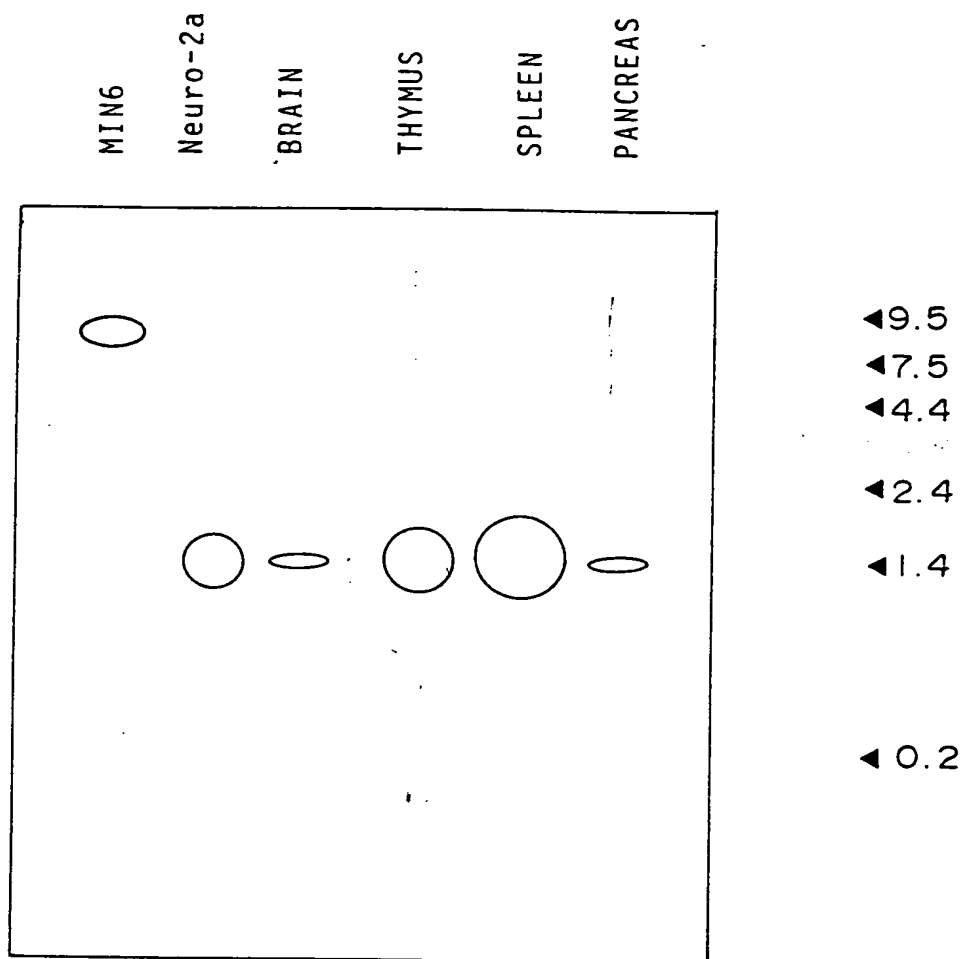
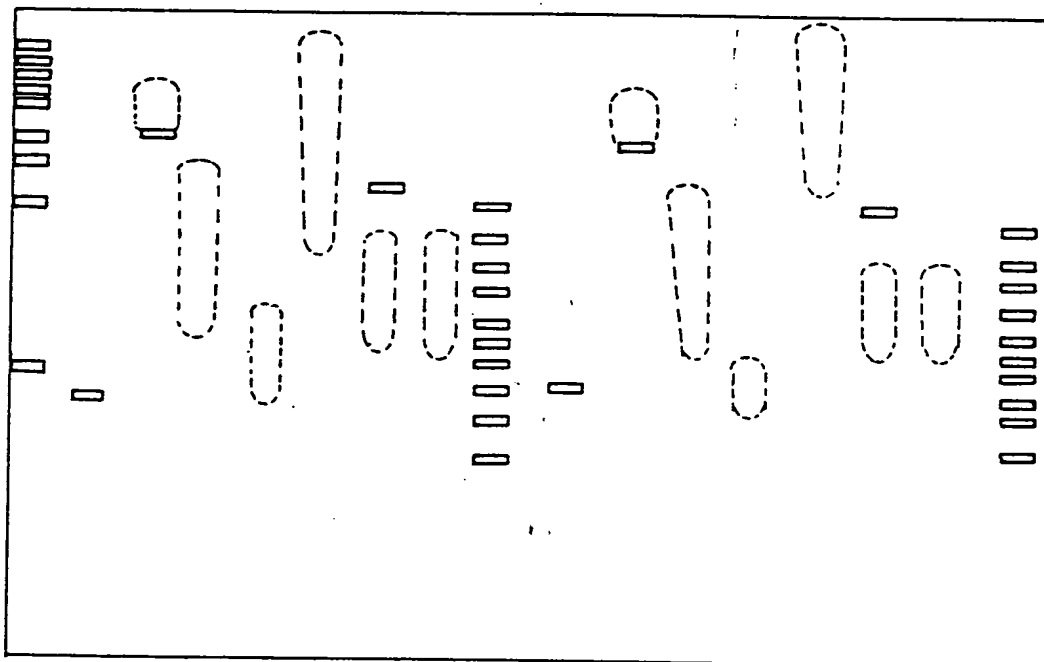


FIGURE 66

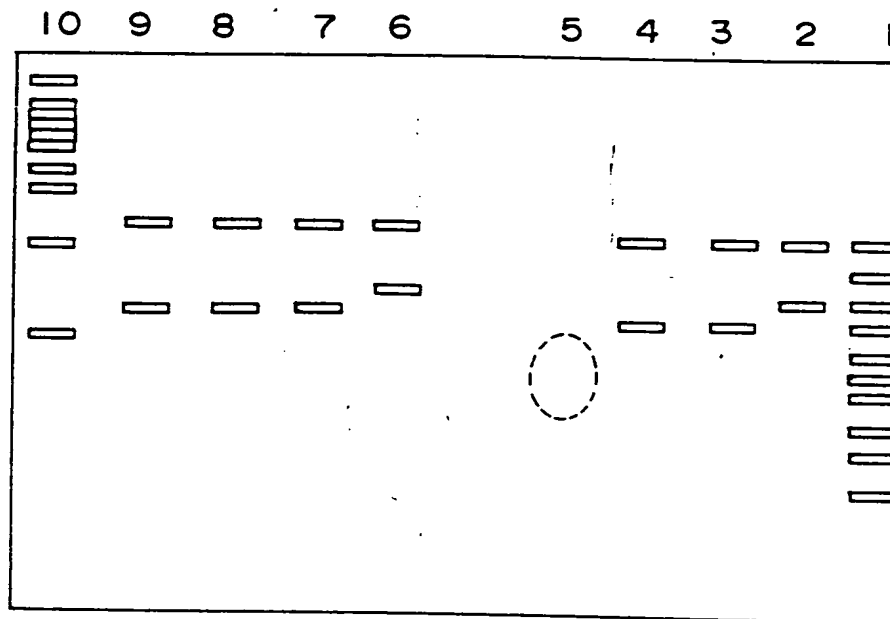
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17



17 16 15 14 13 12 11 10 9 8 7 6 5 4 3 2 1

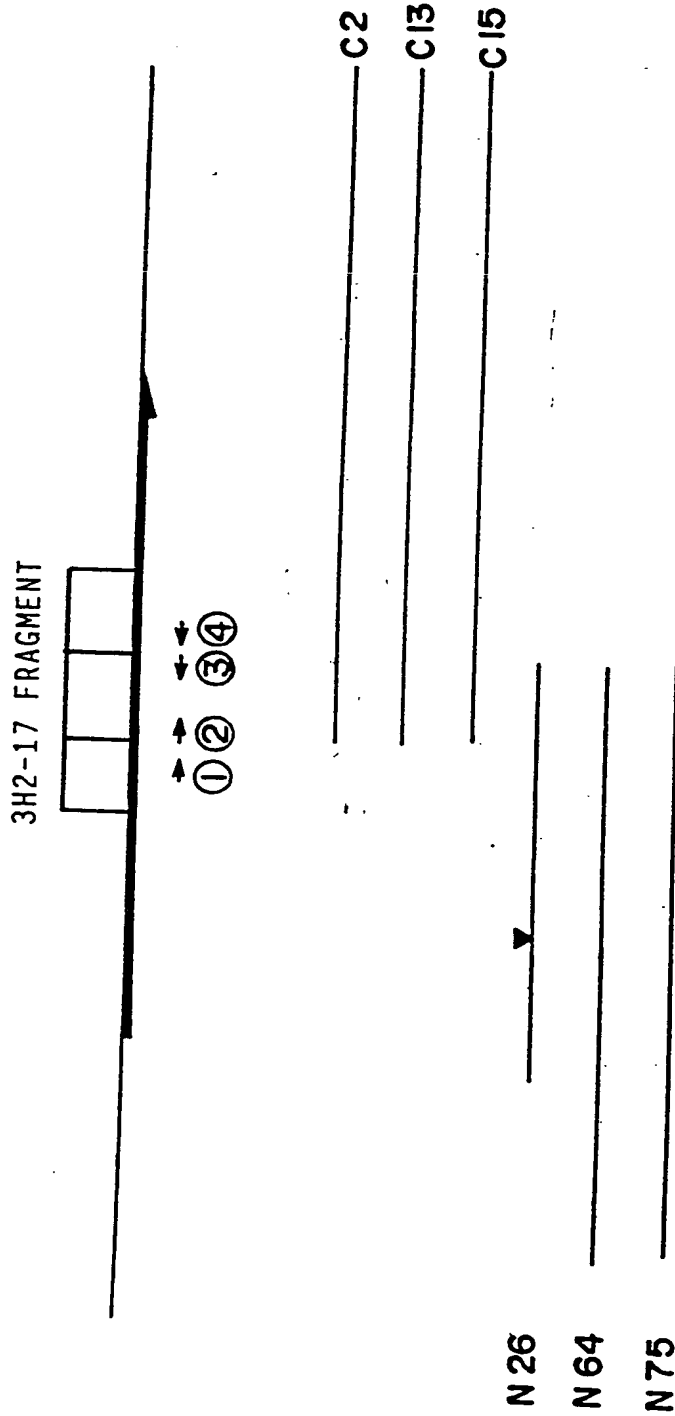
6 7 / 7 9

FIGURE 67



6 7 / 7 9

FIGURE 68



C2 SPLEEN DERIVED C13 C15 THYMUS DERIVED
 N75 SPLEEN DERIVED N26 N64 THYMUS DERIVED
 ▼ PCR ERROR SITE

FIGURE 69

1	GAGCATAGGAAAGGCTGACAGGCAGTTATGGAGCAGGACAATGGCACCATCCAGGCTCCA	60
1	MetGluGlnAspAsnGlyThrIleGlnAlaPro	11
61	GGCTTGCCGCCACCACCTGCGTCTACCGTGAGGATTTCAAGCGACTGCTGCTAACCCCG	120
11	GlyLeuProProThrThrCysValTyrArgGluAspPheLysArgLeuLeuLeuThrPro	31
121	GTATACTCGGTGGTGGTGGTGGTGGCTGCCACTGAACATCTGCGTCATTGCCCCAGATC	180
31	ValTyrSerValValLeuValValGlyLeuProLeuAsnIleCysValIleAlaGlnIle	51
181	TGCGCATCCCGCCGACCCCTGACCCGTCCCGCTGTGTACACCCCTGAACCTGGCACTGGCG	240
51	CysAlaSerArgArgThrLeuThrArgSerAlaValTyrThrLeuAsnLeuAlaLeuAla	71
241	GACCTGATGTATGCTGTTCCTACTACCCCTACTTATCTATAACTACGCCAGAGGGGACCAC	300
71	AspLeuMetTyrAlaCysSerLeuProLeuLeuIleTyrAsnTyrAlaArgGlyAspHis	91
301	TGGCCCTTCGGAGACCTCGCCTGCCGCTTTGTACGCTTCCTCTCTATGCCAATCTACAT	360
91	TrpProPheGlyAspLeuAlaCysArgPheValArgPheLeuPheTyrAlaAsnLeuHis	111
361	GGCAGCATCCTGTTCCTCACCTGCATTAGCTTCCAGCGCTACCTGGGCATCTGCCACCCC	420
111	GlySerIleLeuPheLeuThrCysIleSerPheGlnArgTyrLeuGlyIleCysHisPro	131
421	CTGGCTTCCTGGCACAAGCGTGGAGGTGCGCGTGTGCTTGGGTAGTGTGTGGAGTCGTG	480
131	LeuAlaSerTrpHisLysArgGlyGlyArgArgAlaAlaTrpValValCysGlyValVal	151
481	TGGCTGGCTGTGACAGCCAGTGCCTGCCACGGCAGTCTTTGCTGCCACAGGCATCCAG	540
151	TrpLeuAlaValThrAlaGlnCysLeuProThrAlaValPheAlaAlaThrGlyIleGln	171
541	CGCAACCGCACTGTGTGTACGACCTGAGCCACCCATCCTGTCTACTCGCTACCTGCCC	600
171	ArgAsnArgThrValCysTyrAspLeuSerProProIleLeuSerThrArgTyrLeuPro	191
601	TATGGTATGGCCCTCACGGTCATCGGCTTCTTGCTGCCCTTCATAGCCTTACTGGCTTGT	660
191	TyrGlyMetAlaLeuThrValIleGlyPheLeuLeuProPheIleAlaLeuLeuAlaCys	211
661	TATTGTCCCATGGCCCGCCGCTGTGTGCCAGGATGGCCCAGCAGGTCTGTGGCCCAA	720
211	TyrCysArgMetAlaArgArgLeuCysArgGlnAspGlyProAlaGlyProValAlaGln	231
721	GAGCGGCGCAGCAAGGCGGCTCGTATGGCTGTGGTGGTGGCAGCTGTCTTTGCCATCAGC	780
231	GluArgArgSerLysAlaAlaArgMetAlaValValValAlaAlaValPheAlaIleSer	251
781	TTCTGCTCTTCCACATCACCAGACAGCCTACTTGGCTGTGCGCTCCACGCCCGGTGTC	840
251	PheLeuProPheHisIleThrLysThrAlaTyrLeuAlaValArgSerThrProGlyVal	271
841	TCTTGCCCTGTGCTGGAGACCTTCGCTGCTGCCTACAAAGGCACTCGGCCCTTCGCCAGT	900
271	SerCysProValLeuGluThrPheAlaAlaAlaTyrLysGlyThrArgProPheAlaSer	291
901	GTCAACAGTGTCTCGGACCCCATCTCTTCTACTTCACACAACAGAAGTTCGGCGGCAA	960
291	ValAsnSerValLeuAspProIleLeuPheTyrPheThrGlnGlnLysPheArgArgGln	311
961	CCCCACGATCTCTTACAGAGGCTCACAGCCAAGTGGCAGAGGCAGAGAGTCTGAGGCCCC	1020
311	ProHisAspLeuLeuGlnArgLeuThrAlaLysTrpGlnArgGlnArgVal***	329

FIGURE 70

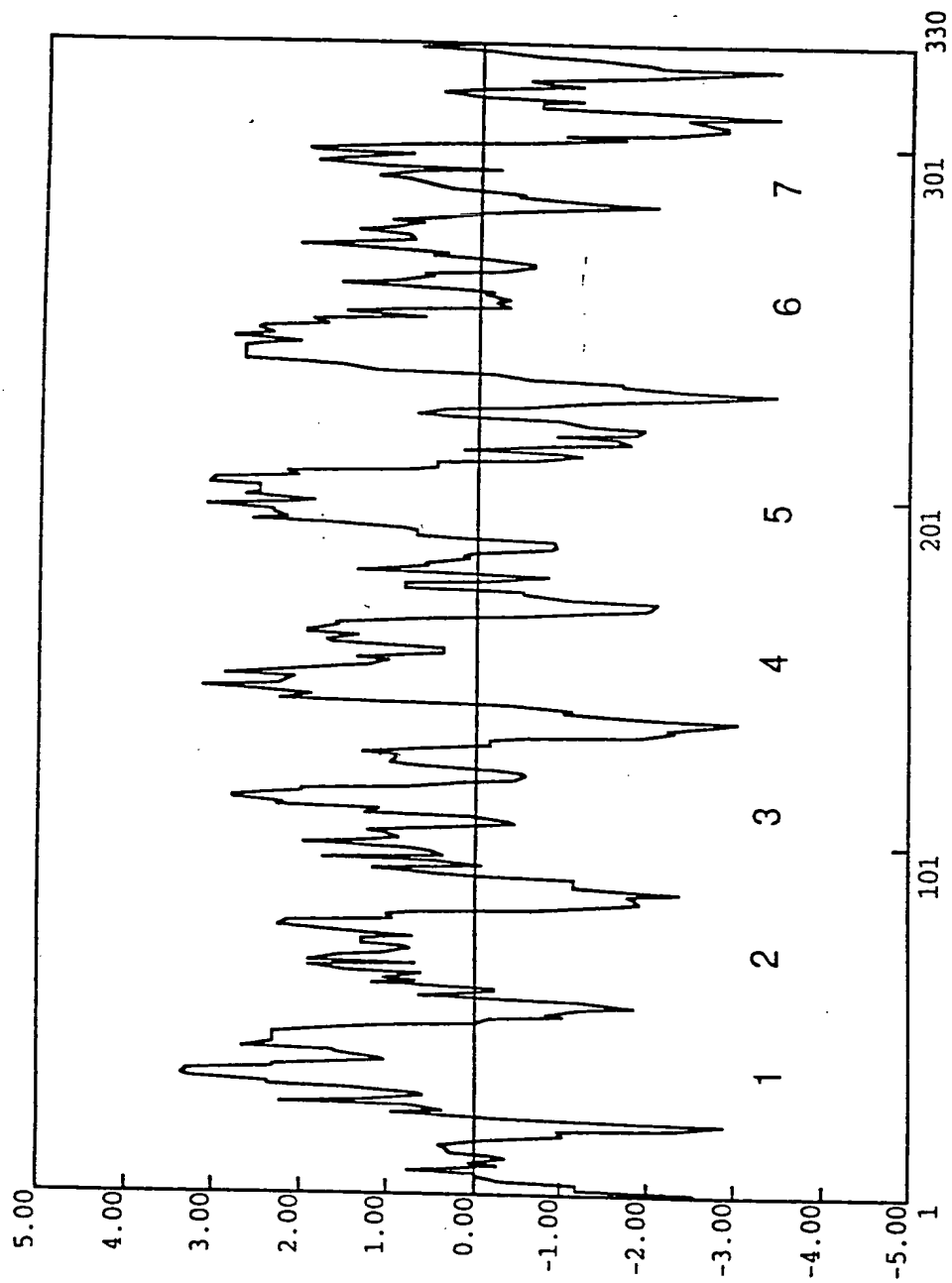


FIGURE 71

75+13, CODING	1	10	20	30	40	50	
P2UR_MOUSE	1	MAADLEFANS	TINGWEGDE	LGY-----	---KGRFN-	DEKVVLLP-	50
P2YR_CHICK	1	ATEALISAAL	---NGT- 2 -EE	ELAGGWAAGN	ATVTKCSLTKT	GEQFYVIL-ET	50
75+13, CODING	51	60	70	80	90	100	
P2UR_MOUSE	51	V-YSVLVVVG	-EPINICVIA	QI--CASRTI	LTR-SAVVIL	NLALADLMYA	100
P2YR_CHICK	51	VSYGVVCTLS	-LCNVALY	-HFLC-RLKI	ANA-SITVME	HLAVSDSLYA	100
	51	V-YILVFTTS	FLG-NSVALW	M-E-VFHMSP	ASGIS-VYME	NLALADFLYV	100
75+13, CODING	101	110	120	130	140	150	
P2UR_MOUSE	101	CSLEPILLYNY	ARG-DHWBEG	ELA-CREVREI	SVANDLSSIL	SLTCTISFORY	150
P2YR_CHICK	101	ASLEPILLYNY	ARG-DHWBES	TVLCKLVREI	SVTNLYCSIL	SLTCTISVHRC	150
	101	LTLEALISFY	FNKTE-NEEG	QVCKLOREI	SHVNLVGSIL	SLTCTISVHRV	150
75+13, CODING	151	160	170	180	190	200	
P2UR_MOUSE	151	EGICHPILASW	HKSCH-SPA	WVCGVVVLA	VTAQCL-EIA	VEFAA-IGTOR	200
P2YR_CHICK	151	EGVLRPLHSL	--RWGRARYA	RRVAAVVVWL	VLA-CQAPVL	YFVT-LSVRG	200
	151	TGVVHPLKSL	G-SLKKGN-A	VYVSSLVVAL	VVAVIA-EIE	-EYSGIGVRR	200
75+13, CODING	201	210	220	230	240	250	
P2UR_MOUSE	201	NRI-VGYDLS	PPI-E-SIRY	LPYCSALIVL	GELLPEIALI	ACVCRMARRI	250
P2YR_CHICK	201	TR-LTCHDAS	ARE-LFSHEV	A-YSSVMLGL	LEAVEFSVIL	VGVVLMARRL	250
	201	NKVTTCYDIT	ACEVRSYEV	--YSHCTIVF	MCIEPPIVIL	GVYGLIVKAL	250
75+13, CODING	251	260	270	280	290	300	
P2UR_MOUSE	251	CRODSPA-GP	VAQERFSKAA	--EAAVVVAA	VEFATSELEPH	ITUKTAMIAVR	300
P2YR_CHICK	251	-LR--PAYSE	TGGDPSAKRK	SVETIALVLA	VEFALCELEPH	VIRITAYYSFR	300
	251	IYKD-LDNEP	---L-PRK--	SIYLVITVLT	VEFASVLEPH	VMKVLENRAR	300
75+13, CODING	301	310	320	330	340	350	
P2UR_MOUSE	301	STP---GVSC	PVLETFAAAY	KGURPESAVN	SVLDBILFYF	TOQKERRRPH	350
P2YR_CHICK	301	STP----LSC	HTLNAINMAY	KGURPLEASAN	SCIDPVIAYEL	AGQRLVRFRAR	350
	301	-LDFQTPQMC	AFNDKVYATY	QVTRGLASLN	SCVDEPILYST	AGOTERRRLS	350
75+13, CODING	351	360	370	380	390	400	
P2UR_MOUSE	351	ELLQRLTAKW	QRQRV*....	400
P2YR_CHICK	351	DAXPTEPTP	SEQARRKGL	HRPNRTVRKD	LSVSSDDSR	TESTPAGSET	400
	351	RAIRKSSRRS	EPNVQSSSE	MILNILLTEYK	QNGDTSL...	400
75+13, CODING	401	410	420	430	440	450	
P2UR_MOUSE	401	450
P2YR_CHICK	401	KDIRL.....	450
	401	450

FIGURE 72

5'	9						18			27			36			45			54		
	GCC	ACC	AAC	GTG	TTC	ATC	CTG	TCA	CTG	GCC	GAT	GTG	CTG	GTG	ACA	GCC	ATC	TGC			
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
										Ala	Asp	Val	Leu	Val	Thr	Ala	Ile	Cys			
	63						72			81			90			99			108		
	CTG	CCG	GCC	AGT	CTG	CTG	GTA	GAC	ATC	ACG	GAA	TCC	TGG	CTC	TTT	GGC	CAT	GCC			
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Leu	Pro	Ala	Ser	Leu	Leu	Val	Asp	Ile	Thr	Glu	Ser	Trp	Leu	Phe	Gly	His	Ala			
	117						126			135			144			153			162		
	CTC	TGC	AAG	GTC	ATC	CCC	TAT	CTA	CAG	GCC	GTG	TCC	GTG	TCA	GTG	GTC	GTG	CTG			
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Leu	Cys	Lys	Val	Ile	Pro	Tyr	Leu	Gln	Ala	Val	Ser	Val	Ser	Val	Val	Val	Leu			
	171						180			189			198			207			216		
	ACT	CTC	AGC	TCC	ATC	GCC	CTG	GAC	CGC	TGG	TAC	GCC	ATC	TGC	CAC	CCG	CTG	TTG			
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Thr	Leu	Ser	Ser	Ile	Ala	Leu	Asp	Arg	Trp	Tyr	Ala	Ile	Cys	His	Pro	Leu	Leu			
	225						234			243			252			261			270		
	TTC	AAG	AGC	ACT	GCC	CGG	CGC	GCC	CGC	GGC	TCC	ATC	CTC	GGC	ATC	TGG	GCG	GTG			
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Phe	Lys	Ser	Thr	Ala	Arg	Arg	Ala	Arg	Gly	Ser	Ile	Leu	Gly	Ile	Trp	Ala	Val			
	279						288			297			306			315			324		
	TCG	CTG	GCT	GTC	ATG	GTG	CCT	CAG	GCT	GCT	GTC	ATG	GAG	TGT	AGC	AGC	GTG	CTG			
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Ser	Leu	Ala	Val	Met	Val	Pro	Gln	Ala	Ala	Val	Met	Glu	Cys	Ser	Ser	Val	Leu			
	333						342			351			360			369			378		
	CCC	GAG	CTG	GCC	AAC	CGC	ACC	CGC	CTC	CTG	TCT	GTC	TGT	GAT	GAG	CGC	TGG	GCA			
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Pro	Glu	Leu	Ala	Asn	Arg	Thr	Arg	Leu	Leu	Ser	Val	Cys	Asp	Glu	Arg	Trp	Ala			
	387						396			405			414			423			432		
	GAC	GAC	CTG	TAC	CCC	AAG	ATC	TAC	CAC	AGC	TGC	TTC	TTC	ATT	GTC	ACC	TAC	CTG			
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Asp	Asp	Leu	Tyr	Pro	Lys	Ile	Tyr	His	Ser	Cys	Phe	Phe	Ile	Val	Thr	Tyr	Leu			
	441						450			459			468			477			486		
	GCC	CCA	CTG	GGC	CTC	ATG	GCC	ATG	GCC	TAT	TTC	CAG	ATC	TTC	CGC	AAG	CTC	TGG			
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Ala	Pro	Leu	Gly	Leu	Met	Ala	Met	Ala	Tyr	Phe	Gln	Ile	Phe	Arg	Lys	Leu	Trp			
	495						504			513			522			531			540		
	GGC	CGC	CAG	ATC	CCC	GGC	ACC	ACC	TCG	GCC	CTG	GTG	CGC	AAC	TGG	AAG	CGG	CCC			

FIGURE 73

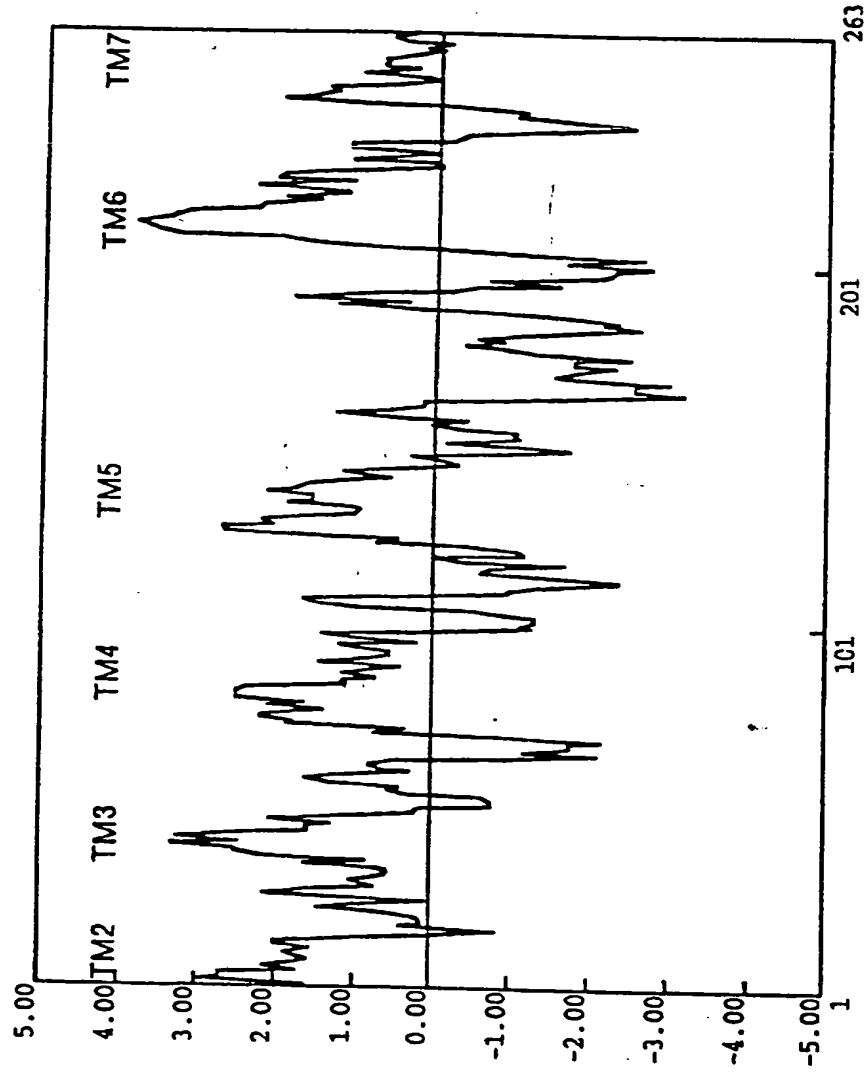
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-----
Gly Arg Gln Ile Pro Gly Thr Thr Ser Ala Leu Val Arg Asn Trp Lys Arg Pro
      549      558      567      576      585      594
TCA GAC CAG CTG GAC GAC CAG GGC CAG GGC CTG AGC TCA GAG CCC CAG CCC CGG
-----
Ser Asp Gln Leu Asp Asp Gln Gly Gln Gly Leu Ser Ser Glu Pro Gln Pro Arg
      603      612      621      630      639      648
GCC CGC GCC TTC CTG GCC GAG GTG AAA CAG ATG CGA GCC CGG AGG AAG ACG GCC
-----
Ala Arg Ala Phe Leu Ala Glu Val Lys Gln Met Arg Ala Arg Arg Lys Thr Ala
      657      666      675      684      693      702
AAG ATG CTG ATG GTG GTG CTG CTG GTC TTC GCC CTC TGC TAC CTG CCC ATC AGT
-----
Lys Met Leu Met Val Val Leu Leu Val Phe Ala Leu Cys Tyr Leu Pro Ile Ser
      711      720      729      738      747      756
GTC CTC AAC GTC CTC AAG AGG GTC TTC GGG ATG TTC CGC CAA GCC AGC GAC CGA
-----
Val Leu Asn Val Leu Lys Arg Val Phe Gly Met Phe Arg Gln Ala Ser Asp Arg
      765      774      783      792      801      810
GAG GCC ATC TAC GCC TGC TTC ACC TTC TCC CAC TGG CTG GTG TAC GCC AAC AGC
-----
Glu Ala Ile Tyr Ala Cys Phe Thr Phe Ser His Trp Leu Val Tyr Ala Asn Ser
      819      828      837
GCC GCC AAT CCC CTC CTC TAC TCC TTC CTC CCT 3'
-----
Ala Ala

```

DATE RECEIVED

FIGURE 74



7 5 / 7 9

FIGURE 75

10 μ M ATP

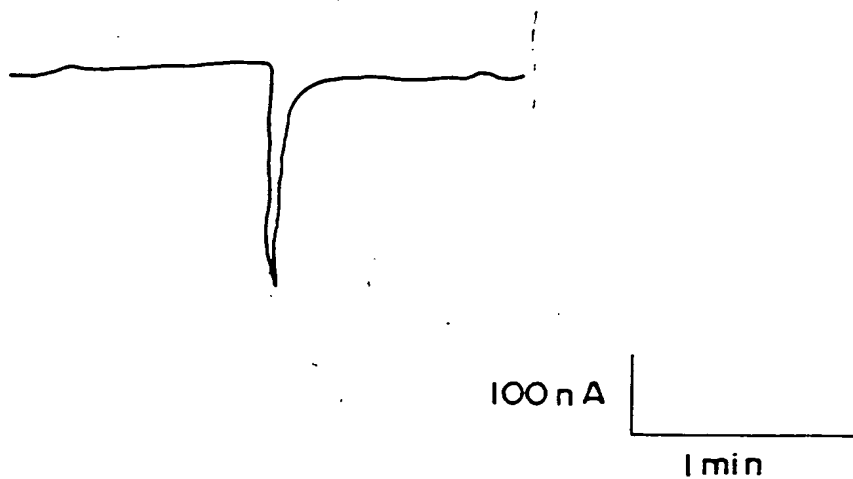


FIGURE 7 6

h3H2-17(5-3)	1	10	20	30	40	50	50
p3H2-17(5')	1	CTGGCCCTGG	TGGGCAACAT	CCTGGCTTCC	TGGCACAAGC	GTGGAGGTGC	50
h3H2-17(5-3)	51	60	70	80	90	100	100
p3H2-17(5')	51	CCGTGCTGCT	TGGGTAGTGT	GTEGAGTCGT	GTGGCTGGCT	GTACATGCG	100
h3H2-17(5-3)	101	110	120	130	140	150	150
p3H2-17(5')	101	AGTGGCTGCG	CACAGGCATC	TTCGCTGCG	CAGGCAATCA	GCGTATGCG	150
h3H2-17(5-3)	151	160	170	180	190	200	200
p3H2-17(5')	151	ACGTCCTGCG	ATGAGCTCAG	CCGCGCTGCC	CTGGCCACCC	ACGATATGCG	200
h3H2-17(5-3)	201	210	220	230	240	250	250
p3H2-17(5')	201	CTATGGCATG	GCTCTCACTG	TCATGGGCTT	CTTCGCTGCG	TTTCTATGCG	250
h3H2-17(5-3)	251	260	270	280	290	300	300
p3H2-17(5')	251	ATGTCGCTG	CTACTCTCTG	CTGGCTGCG	GCG	300
h3H2-17(5-3)	301	310	320	330	340	350	350
p3H2-17(5')	301	CCAGCAGGTC	CTGTGGCCCA	AGAGCGGCG	AGCAAGGCG	CTCGTATGCG	350
h3H2-17(5-3)	351	360	370	380	390	400	400
p3H2-17(5')	351	TGTGGTGGTG	GCAGCTGTCT	TTCGCCCTTG	CTGGCTGCCT	CTCTAC....	400

FIGURE 77

1	TGACTCCCTGAACATAGGAAACCCACCTGGGCAGCCATGGAATGGGACAATGGCACAGGC	60
1	MetGluTrpAspAsnGlyThrGly	8
61	CAGGCTCTGGGCTTGCCACCCACCACCTGTGTCTACCGGAGAACTTCAAGCAACTGCTG	120
8	GlnAlaLeuGlyLeuProProThrThrCysValTyrArgGluAsnPheLysGlnLeuLeu	28
121	CTGCCACCTGTGTATTGGCGGTGCTGGCGGCTGGCCTGCCGCTGAACATCTGTGTCATT	180
28	LeuProProValTyrSerAlaValLeuAlaAlaGlyLeuProLeuAsnIleCysValIle	48
181	ACCCAGATCTGCACGTCCCGCGGGCCCTGACCCGCACGGCCGTGTACACCCTAAACCTT	240
48	ThrGlnIleCysThrSerArgArgAlaLeuThrArgThrAlaValTyrThrLeuAsnLeu	68
241	GCTCTGGCTGACCTGCTATATGCTGCTCCCTGCCCCTGCTCATCTCAACTATGCCCAA	300
68	AlaLeuAlaAspLeuLeuTyrAlaCysSerLeuProLeuLeuIleTyrAsnTyrAlaGln	88
301	GGTGATCACTGGCCCTTTGGCGACTTCGCCTGCCGCTGGTCCGCTTCTCTTCTATGCC	360
88	GlyAspHisTrpProPheGlyAspPheAlaCysArgLeuValArgPheLeuPheTyrAla	108
361	AACCTGCACGGCAGCATCTCTTCTCACCTGCATCAGCTTCCAGCGCTACCTGGGCATC	420
108	AsnLeuHisGlySerIleLeuPheLeuThrCysIleSerPheGlnArgTyrLeuGlyIle	128
421	TGCCACCCGCTGGCCCCCTGGCACAAACGTGGGGGCGCGGGCTGCCTGGCTAGTGTGT	480
128	CysHisProLeuAlaProTrpHisLysArgGlyGlyArgArgAlaAlaTrpLeuValCys	148
481	GTAACCGTGTGGCTGGCCGTGACAACCCAGTGCCTGCCACAGCCATCTTCGCTGCCACA	540
148	ValThrValTrpLeuAlaValThrThrGlnCysLeuProThrAlaIlePheAlaAlaThr	168
541	GGCATCCAGCGTAACCGCACTGTCTGCTATGACCTCAGCCCGCTGCCCTGGCCACCCAC	600
168	GlyIleGlnArgAsnArgThrValCysTyrAspLeuSerProProAlaLeuAlaThrHis	188
601	TATATGCCCTATGGCATGGCTCTCACTGTTCATCGGCTTCCCTGCTGCCCTTTGCTGCCCTG	660
188	TyrMetProTyrGlyMetAlaLeuThrValIleGlyPheLeuLeuProPheAlaAlaLeu	208
661	CTGGCCTGCTACTGTCTCCTGGCCTGCCGCTGTGCCGCCAGGATGGCCCGGCAGAGCCT	720
208	LeuAlaCysTyrCysLeuLeuAlaCysArgLeuCysArgGlnAspGlyProAlaGluPro	228
721	GTGGCCCAGGAGCGGCGTGGCAAGGCGGCCGCGCATGGCCGTGGTGGTGGCTGCTGCCTTT	780
228	ValAlaGlnGluArgArgGlyLysAlaAlaArgMetAlaValValAlaAlaAlaPhe	248
781	GCCATCAGCTTCCTGCCTTTTCACATCACAAGACAGCCTACCTGGCAGTGGGCTCGACG	840
248	AlaIleSerPheLeuProPheHisIleThrLysThrAlaTyrLeuAlaValGlySerThr	268
841	CCGGGCGTCCCTGCACTGTATTGGAGGCTTTTGACGGCCTACAAAGGCACGCGGCCG	900
268	ProGlyValProCysThrValLeuGluAlaPheAlaAlaAlaTyrLysGlyThrArgPro	288
901	TTTGCCAGTGCCAACAGCGTGTGGACCCCATCTCTTCTACTTCACCCAGAAGAAGTTC	960
288	PheAlaSerAlaAsnSerValLeuAspProIleLeuPheTyrPheThrGlnLysLysPhe	308
961	CGCCGGCGACCACATGAGCTCCTACAGAACTCACAGCCAAATGGCAGAGGCAGGGTCGC	1020
308	ArgArgArgProHisGluLeuLeuGlnLysLeuThrAlaLysTrpGlnArgGlnGlyArg	328
1021	TGA	1023
328	***	329

FIGURE 78

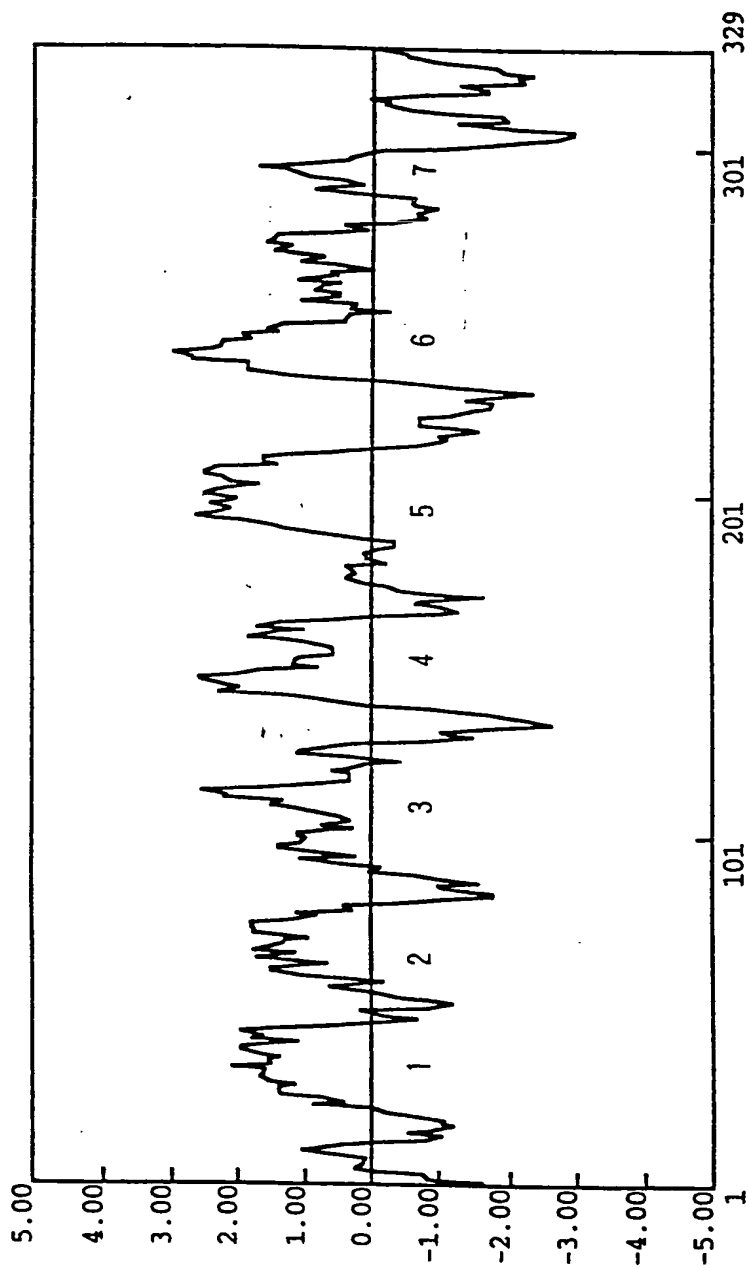


FIGURE 79

human prino, mouseFULL3H2	1	MEVDNGTGOA	10	LGLPPTTCVY	20	RENEKQLLLP	30	PVYSATLAAG	40	LPLNICVITG	50
	1	MEQDNGTGOA		PGLPPTTCVY		REDEKRLLLT		PVYSVTLVVG		LPLNICVITG	50
human prino, mouseFULL3H2	51	ICPSRRALTR	60	TAVTINLAL	70	ADLLYACSLP	80	LLIYNVAGCD	90	HWPFQDFACR	100
	51	ICASRRILTR		SAVTINLAL		ADLLYACSLP		LLIYNVARGD		HWPFQDFACR	100
human prino, mouseFULL3H2	101	LVRFLFYANL	110	HGSILFLTCI	120	SFORVLGICH	130	PLAPWHKRGG	140	RRAAWVVCVT	150
	101	FVRFLFYANL		HGSILFLTCI		SFORVLGICH		PLASWHKRGG		RRAAWVVC5V	150
human prino, mouseFULL3H2	151	VMLAVTIQCL	160	PTAIEAATGI	170	QRNRTVCYDL	180	SPPALATHYM	190	PYGNALTVIG	200
	151	VMLAVTAQCL		PTAIEAATGI		QRNRTVCYDL		SPPILSTRYL		PYGNALTVIG	200
human prino, mouseFULL3H2	201	FLLPFAALLA	210	CYCLLECLC	220	RODGPAGEVA	230	QERRSKAARM	240	AVWVAAFAT	250
	201	FLLPFAALLA		CYCRMARRLC		RODGPAGEVA		QERRSKAARM		AVWVAAFAT	250
human prino, mouseFULL3H2	251	SFLPFHITKT	260	AYLAVGSTFG	270	VPCLVLEAFA	280	AAVKGTRPFA	290	SANSVLDPIL	300
	251	SFLPFHITKT		AYLAVRSTFG		VSCPVLETPA		AAVKGTRPFA		SANSVLDPIL	300
human prino, mouseFULL3H2	301	FVFTQCKFRR	310	RPHLLQALTL	320	AKWQRCR*	330	340	350
	301	FVFTQCKFRR		QPHDLLQALTL		AKWQRCRV*		350